





PRIOR FILING DATE: 1998-10-14  
 PRIOR APPLICATION NUMBER: 60/104987  
 PRIOR FILING DATE: 1998-10-20  
 PRIOR APPLICATION NUMBER: 60/105000  
 PRIOR FILING DATE: 1998-10-20  
 PRIOR APPLICATION NUMBER: 60/105002  
 PRIOR FILING DATE: 1998-10-20  
 PRIOR APPLICATION NUMBER: 60/105104  
 PRIOR FILING DATE: 1998-10-21  
 PRIOR APPLICATION NUMBER: 60/105169  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105266  
 PRIOR FILING DATE: 1998-10-22  
 PRIOR APPLICATION NUMBER: 60/105693  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105694  
 PRIOR FILING DATE: 1998-10-26  
 PRIOR APPLICATION NUMBER: 60/105807

Query Match 100.0%; Score 989; DB 10; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-226;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60  
 DB 1 GCGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60  
 QY 61 TCCCGCGGCTCTGCGCCGCGCATGACCCAGCGGTGCCCCGCTCTCCGTGCCCCGCG 120  
 DB 61 TCCCGCGGCTCTGCGCCGCGCATGACCCAGCGGTGCCCCGCTCTCCGTGCCCCGCG 120  
 QY 121 CGCTGACCTTGAGCTGAGCGGCACTGAGCGCGCTTCCGCACTGGCTCTTCTGAGGA 180  
 DB 121 CGCTGACCTTGAGCTGAGCGGCACTGAGCGCGCTTCCGCACTGGCTCTTCTGAGGA 180  
 QY 181 GGGGGTCCCCCATATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 DB 181 GGGGGTCCCCCATATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 QY 241 GCGTGTGAGATATCTTCTGAGCGGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 DB 241 GCGTGTGAGATATCTTCTGAGCGGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 QY 301 GGGTGTGACCTCTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 DB 301 GGGTGTGACCTCTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 QY 361 TCTTGCGCAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 DB 361 TCTTGCGCAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 QY 421 CGGCGTACTCCGCGCTGAGCGGCTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 DB 421 CGGCGTACTCCGCGCTGAGCGGCTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 QY 481 GCGAGGTGAGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
 DB 481 GCGAGGTGAGCCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540  
 QY 541 AGCACAAGATCGACCTCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600  
 DB 541 AGCACAAGATCGACCTCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600  
 QY 601 CGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
 DB 601 CGGCGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660  
 QY 661 CCTACTAGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
 DB 661 CCTACTAGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 720  
 QY 721 TCTGTGCGGCGGAGAGGTGTGCACTCCGAAAGGCGAGCGTGGCGGCGGAGGTGTGTC 780  
 DB 721 TCTGTGCGGCGGAGAGGTGTGCACTCCGAAAGGCGAGCGTGGCGGCGGAGGTGTGTC 780

DB 721 TCTGTGCGGCGGAGAGGTGTGCACTCCGAAAGGCGAGCGTGGCGGCGGAGGTGTGTC 780  
 QY 781 GAAACCTAAAGAGCGATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840  
 DB 781 GAAACCTAAAGAGCGATCCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840  
 QY 841 GCGATGACTACCTTGCGCTTCAAGATCTAGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGG 900  
 DB 841 GCGATGACTACCTTGCGCTTCAAGATCTAGGCGTGGCGGCGGCGGCGGCGGCGGCGGCGG 900  
 QY 901 GAGGTTGCTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960  
 DB 901 GAGGTTGCTGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 960  
 QY 961 GCTGGACACAAAAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 989  
 DB 961 GCTGGACACAAAAAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 989

## RESULT 2

US-10-307-817-121  
 ; Sequence 121, Application US/10307817  
 ; Publication No. US20040058338A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Agere et al.  
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME  
 ; FILE REFERENCE: 21402-502C  
 ; CURRENT APPLICATION NUMBER: US/10/307,817  
 ; NUMBER OF SEQ ID NOS: 682  
 ; SOFTWARE: Cursesqlist version 0.1  
 ; SEQ ID NO 121  
 ; LENGTH: 989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: CDS  
 ; LOCATION: (84)..(869)  
 US-10-307-817-121

Query Match 100.0%; Score 989; DB 12; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-226;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60  
 DB 1 GCGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60  
 QY 61 TCCCGCGGCTCTGCGCCGCGCATGACCCAGCGGTGCCCCGCTCTCCGTGCCCCGCG 120  
 DB 61 TCCCGCGGCTCTGCGCCGCGCATGACCCAGCGGTGCCCCGCTCTCCGTGCCCCGCG 120  
 QY 121 CGCTGACCTTGAGCTGAGCGGCACTGAGCGGCTTCCGCACTGGCTCTTCTGAGGA 180  
 DB 121 CGCTGACCTTGAGCTGAGCGGCACTGAGCGGCTTCCGCACTGGCTCTTCTGAGGA 180  
 QY 181 GGGGGTCCCCCATATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 DB 181 GGGGGTCCCCCATATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240  
 QY 241 GCGTGTGAGATATCTTCTGAGCGGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 DB 241 GCGTGTGAGATATCTTCTGAGCGGCTCATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300  
 QY 301 GGGTGTGACCTCTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 DB 301 GGGTGTGACCTCTGAGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360  
 QY 361 TCTTGCGCAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 DB 361 TCTTGCGCAACCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420  
 QY 421 CGGCGTACTCCGCGCTGAGCGGCTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 480  
 DB 421 CGGCGTACTCCGCGCTGAGCGGCTGAGCGGCTGAGCGGCGGCGGCGGCGGCGGCGGCGG 480



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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C14
; CURRENT APPLICATION NUMBER: US/10/006,856A
; NUMBER OF SEQ ID NOS: 477
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 305
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-856A-305

```

Query Match 100.0%; Score 989; DB 14; Length 989;

Best Local Similarity 100.0%; Pred. No. 5,6e-226; Mismatches 0; Indels 0; Gaps 0;

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; Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60
DB 1 GCGGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60
QY 61 TCCCGCGGCTCTGCGCCCGGCGCATGACCGCGGTGCGCCGCTCTCCGTCGCCCGCG 120
DB 61 TCCCGCGGCTCTGCGCCCGGCGCATGACCGCGGTGCGCCGCTCTCCGTCGCCCGCG 120
QY 121 CGCTGGCCCTGGGCTCAGCGCGGACTGGGCGCGCTTCGCACTGGCTCTTCTCGGGA 180
DB 121 CGCTGGCCCTGGGCTCAGCGCGGACTGGGCGCGCTTCGCACTGGCTCTTCTCGGGA 180
QY 181 GGGGGTGGCCCCCATGAGGCGGCGGAGAGAGTGTCTGCTTCCCCCGAGAGACAGCC 240
DB 181 GGGGGTGGCCCCCATGAGGCGGCGGAGAGAGTGTCTGCTTCCCCCGAGAGACAGCC 240
QY 241 GCGTGGAGAGTATCTTCTGAGCGGCTCCATGCGGAGACCGCGGCGCTCGAGAGCTGA 300
DB 241 GCGTGGAGAGTATCTTCTGAGCGGCTCCATGCGGAGACCGCGGCGCTCGAGAGCTGA 300
QY 301 GCGTGGAGAGTATCTTCTGAGCGGCTCCATGCGGAGACCGCGGCGCTCGAGAGCTGA 360
DB 301 GCGTGGAGAGTATCTTCTGAGCGGCTCCATGCGGAGACCGCGGCGCTCGAGAGCTGA 360
QY 361 TCTTGGGCAACCTGGGCGGCTCATGAGGCGCAAGAGGCGTGGAGCTGGGCACTTGA 420
DB 361 TCTTGGGCAACCTGGGCGGCTCATGAGGCGCAAGAGGCGTGGAGCTGGGCACTTGA 420
QY 421 CGGAGTATCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 480
DB 421 CGGAGTATCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTG 480
QY 481 GCGAGTGGAGCGCGGAGCGCGCGGAGTGGAGCGCGCGCTGCGGAGCGCGGAGCGCG 540
DB 481 GCGAGTGGAGCGCGGAGCGCGCGGAGTGGAGCGCGCGCTGCGGAGCGCGGAGCGCG 540
QY 541 AGCACAAGATCGACTTCCGCTGAAGCGCTTGGAGACCTTGAAGAGCTGCTGCGCG 600
DB 541 AGCACAAGATCGACTTCCGCTGAAGCGCTTGGAGACCTTGAAGAGCTGCTGCGCG 600
QY 601 CGGAGGAGCGCGGAGCTTGAAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 660
DB 601 CGGAGGAGCGCGGAGCTTGAAGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCG 660
QY 661 CCTACTGAGCGCTGCTGAGTGGAGCGCGGAGAGCTTCCGCTGCTGAGAG 720
DB 661 CCTACTGAGCGCTGCTGAGTGGAGCGCGGAGAGCTTCCGCTGCTGAGAG 720
QY 721 TCTGTGGCGCGGAGAGTGTCTGCAACTTCCGAAAGGAGAGTGGCGCGGAGTGTGTC 780

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DB 721 TCTGTGGCGCGGAGAGTGTCTGCAACTTCCGAAAGGAGAGTGGCGCGGAGTGTGTC 780
QY 781 GAAACCTTAAGAGAGCGATCCGCGGAGAGCTGAGGCTCATGAGCTCTGCTGCCCTGG 840
DB 781 GAAACCTTAAGAGAGCGATCCGCGGAGAGCTGAGGCTCATGAGCTCTGCTGCCCTGG 840
QY 841 GCGATGAGCTACCTTGGCTTCAAGATCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 900
DB 841 GCGATGAGCTACCTTGGCTTCAAGATCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 900
QY 901 GAGGATGCTGAGGAGCGCGGAGAGTGAAGCTGAGTGAATTTAAATGAAATTAAGTGG 960
DB 901 GAGGATGCTGAGGAGCGCGGAGAGTGAAGCTGAGTGAATTTAAATGAAATTAAGTGG 960
QY 961 GCTGGAGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 989
DB 961 GCTGGAGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 989

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RESULT 5

US-10-006-818A-305

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; Sequence 305, Application US/10006818A
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2830P1C4
; CURRENT APPLICATION NUMBER: US/10/006,818A
; CURRENT FILING DATE: 2001-12-06
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 305
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-006-818A-305

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Query Match 100.0%; Score 989; DB 14; Length 989;

Best Local Similarity 100.0%; Pred. No. 5,6e-226; Mismatches 0; Indels 0; Gaps 0;

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; Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60
DB 1 GCGGGCCCCGAGTCCGAGACCTGTCCAGAGCTCCAGCTCACTGACCTGTCACTGCC 60
QY 61 TCCCGCGGCTCTGCGCCCGGCGCATGACCGCGGTGCGCCGCTCTCCGTCGCCCGCG 120
DB 61 TCCCGCGGCTCTGCGCCCGGCGCATGACCGCGGTGCGCCGCTCTCCGTCGCCCGCG 120
QY 121 CGCTGGCCCTGGGCTCAGCGCGGACTGGGCGCGCTTCGCACTGGCTCTTCTCGGGA 180
DB 121 CGCTGGCCCTGGGCTCAGCGCGGACTGGGCGCGCTTCGCACTGGCTCTTCTCGGGA 180
QY 181 GCGGATGCTACCTTGGCTTCAAGATCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 900
DB 181 GCGGATGCTACCTTGGCTTCAAGATCTAGGCTGAGGCTGAGGCTGAGGCTGAGG 900
QY 901 GAGGATGCTGAGGAGCGCGGAGAGTGAAGCTGAGTGAATTTAAATGAAATTAAGTGG 960
DB 901 GAGGATGCTGAGGAGCGCGGAGAGTGAAGCTGAGTGAATTTAAATGAAATTAAGTGG 960
QY 961 GCTGGAGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 989
DB 961 GCTGGAGACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 989

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Dd		241	GCGTGTGGACGATCTTTTGAGCCGGTCATCGGGAGAACCAGCCGCTGGGAAGCCTGA	3000
Qy		301	GGCTGTGCAGCCCTGGAGCAAGCCGCAAGGGGATTCTATGATGACTGTGGAGAGGCCACG	3600
Dd		301	GGCTGTGCAGCCCTGGAGCAAGCCGCAAGGGGATTCTATGATGACTGTGGAGAGGCCACG	3600
Qy		361	TCTTGGCCAACCTGGCGGCGCTCATCAGGCCAAGAGCGCTGAGCCTGGACACTTCA	4200
Dd		361	TCTTGGCCAACCTGGCGGCGCTCATCAGGCCAAGAGCGCTGAGCCTGGACACTTCA	4200
Qy		421	CGGGCTACTCCGCCCCCTGGCCCTGAGCCCTGGCGCTGCCCGCGGACGGGGCGCTGTGACT	4800
Dd		421	CGGGCTACTCCGCCCCCTGGCCCTGAGCCCTGGCGCTGCCCGCGGACGGGGCGCTGTGACT	4800
Qy		481	GCGAGGTGAACGCGCAGACCCCAGCACTGGACAAGCCCTGTGGAGAGCAGGCCAGAGCGG	5400
Dd		481	GCGAGGTGAACGCGCAGACCCCAGCACTGGACAAGCCCTGTGGAGAGCAGGCCAGAGCGG	5400
Qy		541	AGCAACAAGATCGAACCTCCGGCTGAAACCCGCTTGAGAGACCTTGAGACGAGCTGTGGCG	6000
Dd		541	AGCAACAAGATCGAACCTCCGGCTGAAACCCGCTTGAGAGACCTTGAGACGAGCTGTGGCG	6000
Qy		601	CGGGCGAGCGCGGACCACTTGAAGTGGCCGTGGTAGATGCGGACAAAGAGAACTGCTCG	6600
Dd		601	CGGGCGAGCGCGGACCACTTGAAGTGGCCGTGGTAGATGCGGACAAAGAGAACTGCTCG	6600
Qy		661	CGTAATAAGAGCGCTGCTGAGACGTGCTGGACCCGAGAGGATCCTGGCGCGCTCCCTCAG	7200
Dd		661	CGTAATAAGAGCGCTGCTGAGACGTGCTGGACCCGAGAGGATCCTGGCGCGCTCCCTCAG	7200
Qy		721	TCTGTGGCGCGGGAAGGTGTGCAACTCCGAAAAGGGGACGTGGCGGCGAGTGTGTG	7800
Dd		721	TCTGTGGCGCGGGAAGGTGTGCAACTCCGAAAAGGGGACGTGGCGGCGAGTGTGTG	7800
Qy		781	GAAACCTAAACGAAGCATCCGCGCGGGAAGCTGAGGGTCTACATCAGCCTCGTGCCCTCG	8400
Dd		781	GAAACCTAAACGAAGCATCCGCGCGGGAAGCTGAGGGTCTACATCAGCCTCGTGCCCTCG	8400
Qy		841	GCGATGACTCACCTTGGCCTTCAAGATTAAGGCTGGCCCTCACTAGTGTGGTCTGAGG	9000
Dd		841	GCGATGACTCACCTTGGCCTTCAAGATTAAGGCTGGCCCTCACTAGTGTGGTCTGAGG	9000
Qy		901	GAGGGTGGCTGGGGAACCCGAGAAATGAGCCCTGAAGTTTAAATTGAAAATTAAGTGG	9600
Dd		901	GAGGGTGGCTGGGGAACCCGAGAAATGAGCCCTGAAGTTTAAATTGAAAATTAAGTGG	9600
Qy		961	GCTGGGACACAAAAAATTTTTTTTTTAAAAA 989	
Dd		961	GCTGGGACACAAAAAATTTTTTTTTTAAAAA 989	
RESULT 6				
US-10-015-393A-305				
Sequence 305, Application US/10015393A				
Publication No. US20030069179A1				
GENERAL INFORMATION:				
APPLICANT: Baker, Kevin P.				
APPLICANT: Botstein, David				
APPLICANT: Desnovers, Luc				
APPLICANT: Eason, Dan J.				
APPLICANT: Ferrara, Napoleone				
APPLICANT: Fong, Sherman				
APPLICANT: Gao, Wei-Qiang				
APPLICANT: Goddard, Audrey				
APPLICANT: Godowski, Paul J.				
APPLICANT: Grimaldi, Christopher J.				
APPLICANT: Gurney, Austin L.				
APPLICANT: Hillan, Kenneth J.				
APPLICANT: Pan, James				
APPLICANT: Paoni, Nicholas F.				
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic				
Acids Encoding the Same				

[illegible]

Db 841 GCGATGACCTACCTTGCCCTTCAAGATCTAGAGCTGCCCCCTAGTAGTGCGCTCGAGG 900  
 QY 901 GAGGATTCCTGGAGACCCGAGAAATTGACCTTGAGTTTAAATTCGAAATAAAGTGGG 960  
 Db 901 GAGGATTCCTGGAGACCCGAGAAATTGACCTTGAGTTTAAATTCGAAATAAAGTGGG 960  
 QY 961 GCTGGGACACAAAAAATAAATAAATAA 989  
 Db 961 GCTGGGACACAAAAAATAAATAAATAA 989

## RESULT 7

US-10-015-869A-305  
 ; Sequence 305, Application US/10015869A  
 ; Publication No. US20030073130A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2830P1C45  
 ; CURRENT APPLICATION NUMBER: US/10/015.869A  
 ; CURRENT FILING DATE: 2002-06-25  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 305  
 ; LENGTH: 989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-015-869A-305

Query Match 100.0%; Score 989; DB 14; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5,6e-226;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCGCGGAGCTCGAGACTGTCCAGAGCTCCAGACTCCAGCTGCACTGCTGCTGCG 60  
 Db 1 GCGGCGCGCGGAGCTCGAGACTGTCCAGAGCTCCAGAGCTCCAGCTGCACTGCTGCTGCG 60  
 QY 61 TCCGCGCGCTCTCTGCGCGCGCATGACCCAGCCGCGTGCCTCTCTGCGCGCGCG 120  
 Db 61 TCCGCGCGCTCTCTGCGCGCGCATGACCCAGCCGCGTGCCTCTCTGCGCGCGCG 120  
 QY 121 CGCTGGCGCTGGGCTGAGCCGCACTGGGCGCGCTTGGCACTGGGCTTCTTCTGGGA 180  
 Db 121 CGCTGGCGCTGGGCTGAGCCGCACTGGGCGCGCTTGGCACTGGGCTTCTTCTGGGA 180  
 QY 121 CGCTGGCGCTGGGCTGAGCCGCACTGGGCGCGCTTGGCACTGGGCTTCTTCTGGGA 180  
 Db 121 CGCTGGCGCTGGGCTGAGCCGCACTGGGCGCGCTTGGCACTGGGCTTCTTCTGGGA 180  
 QY 181 GGGGCTGCCCCCATGAGCGAGCGCGAGAGAGTGCCTGCTTCCCGCCGAGACAGCC 240  
 Db 181 GGGGCTGCCCCCATGAGCGAGCGCGAGAGAGTGCCTGCTTCCCGCCGAGACAGCC 240  
 QY 241 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 Db 241 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 QY 301 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 Db 301 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 QY 301 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 Db 301 GCGTGGCGAGTATCTTCTTGAAGCGCTCCCATGCGGAGAGACCCGCGCTGCGAAAGCTTA 300  
 QY 361 TCTTGGCAACCTGGCGCGCTCATCGAGCCAAAGAGGCTGAGACTGGGCACTTCA 420  
 Db 361 TCTTGGCAACCTGGCGCGCTCATCGAGCCAAAGAGGCTGAGACTGGGCACTTCA 420

Db 361 TCTTGGCAACCTGGCGCGCTCATCGAGCCAAAGAGGCTGAGACTGGGCACTTCA 420  
 QY 421 CGGCTACTCGCCCTGCGCCTGCGCTGCGCTGCGCTGCGCGAGCGCGCTGAGCT 480  
 Db 421 CGGCTACTCGCCCTGCGCCTGCGCTGCGCTGCGCTGCGCGAGCGCGCTGAGCT 480  
 QY 481 GCGAGTGAAGCGAGCG 540  
 Db 481 GCGAGTGAAGCGAGCG 540  
 QY 541 AGCACAATGACCTCCGCTGAGAGCCGCGCTTGAAGACCTTGAACAGAGCTGCGCGG 600  
 Db 541 AGCACAATGACCTCCGCTGAGAGCCGCGCTTGAAGACCTTGAACAGAGCTGCGCGG 600  
 QY 601 CGGCGAGCGCGCGCCTTCAAGCTGCGCGCTGCGCGCTGCGCGAGAGAGAGAGAG 660  
 Db 601 CGGCGAGCGCGCGCCTTCAAGCTGCGCGCTGCGCGCTGCGCGAGAGAGAGAGAG 660  
 QY 661 CCTACTAGAGCGCTGCGAGAGCTGCGAGAGCGCGAGAGAGAGAGAGAGAGAGAG 720  
 Db 661 CCTACTAGAGCGCTGCGAGAGCTGCGAGAGCGCGAGAGAGAGAGAGAGAGAGAG 720  
 QY 721 TCTTGGCGCGCGAGAGCTGCAACCTCCGAAAGGAGAGAGAGAGAGAGAGAGAG 780  
 Db 721 TCTTGGCGCGCGAGAGCTGCAACCTCCGAAAGGAGAGAGAGAGAGAGAGAGAG 780  
 QY 781 GAAACCTTAAAG 840  
 Db 781 GAAACCTTAAAG 840  
 QY 841 GCGATGACCTACCTTGGCCTTCAAGATCTAGAGCTGCGCCTTATGATGAGTGCAGG 900  
 Db 841 GCGATGACCTACCTTGGCCTTCAAGATCTAGAGCTGCGCCTTATGATGAGTGCAGG 900  
 QY 901 GAGGATTCCTGGAGACCCGAGAAATTGACCTTGAATTTAAATTCGAAATAAAGTGG 960  
 Db 901 GAGGATTCCTGGAGACCCGAGAAATTGACCTTGAATTTAAATTCGAAATAAAGTGG 960  
 QY 961 GCTGGGACACAAAAAATAAATAAATAA 989  
 Db 961 GCTGGGACACAAAAAATAAATAAATAA 989

## RESULT 8

US-10-012-121A-305  
 ; Sequence 305, Application US/10012121A  
 ; Publication No. US20030073810A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnovers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoni, Nicholas F.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE REFERENCE: P2830P1C20  
 ; CURRENT APPLICATION NUMBER: US/10/012.121A  
 ; CURRENT FILING DATE: 2001-12-07  
 ; Prior Application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 477  
 ; SEQ ID NO 305  
 ; LENGTH: 989  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens

Thu Apr 15 09:23:56 2004

us-10-017-407a-305.rnpb

Page 8

US-10-012-121A-305

Query Match 100.0%; Score 989; DB 14; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5.5e-226;  
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 121 CGCTGAGCCCTGAGGCTCAGCGCCGCTGAGCGCGCGCTTCCGACCTGAGCTTCC 180
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Feng, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2830P15
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Query Match 100.0%; Score 989; DB 14; Length 989;  
Best Local Similarity 100.0%; Pred. No. 5,6e-226; Indels 0; Gaps 0;  
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Db 121 CGTGGCCCTGGGCTCAGCCGCACTGGGCGCGGCTTTCGCCACTGGGCTTCTTCTGGGGA 180  
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 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan I.  
 ; APPLICANT: Ferrara, Napoleone  
 ; APPLICANT: Fong, Sherman  
 ; APPLICANT: Gao, Wei-Qiang  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.  
 ; APPLICANT: Gurney, Austin J.  
 ; APPLICANT: Hillan, Kenneth J.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Paoletti, Nicholas P.  
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 ; FILE OF INVENTION: Acids Encoding the Same  
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 ; PRIOR FILING DATE: 2002-03-19  
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 ; NUMBER OF SEQ ID NOS: 477  
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 ; TYPE: DNA  
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 US-10-006-117A-305  
 Query Match 100.0%; Score 989; DB 14; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-226; Indels 0; Gaps 0;  
 Matches 989; Conservative 0; Mismatches 0;

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DB	241	GCTGTGAGCATATCTTCTGAGCCGCTTCATGCGGAGACACCCGCGCGCTGCGAGACCTTGA	300	
QY	301	GAGCTGATCACCCTGAGAGAGCGCGAGGAGGATTCATATGATGACCTGCGAGAGAGCGCCAGC	360	
DB	301	GAGCTGATCACCCTGAGAGAGCGCGAGGAGGATTCATATGATGACCTGCGAGAGAGCGCCAGC	360	
QY	361	TCTTGCCCAACTGAGCGCGGCTCATTCAGGTCGAGAGAGCGCTGAGACTTGAGCACTTTCA	420	
DB	361	TCTTGCCCAACTGAGCGCGGCTCATTCAGGTCGAGAGAGCGCTGAGACTTGAGCACTTTCA	420	
QY	421	CGGCTATATCCGCGCCCTGAGCCCTGAGCGCTGAGCGCGAGAGCGCGCGCTGAGTACT	480	
DB	421	CGGCTATATCCGCGCCCTGAGCGCTGAGCGCTGAGCGCGAGAGCGCGCGCTGAGTACT	480	
QY	481	GCGAGGTGAGCGCGAGCGCCCGCGAGTGGAGCGGCCCTGTGAGGCGAGGCGCGAGCGG	540	
DB	481	GCGAGGTGAGCGCGAGCGCCCGCGAGTGGAGCGGCCCTGTGAGGCGAGGCGCGAGCGG	540	
QY	541	AGCACAATATGACCTCCGCGCTGAAAGCCCGCTTGGAGACCTCTGAGACAGCTGTGAGCGG	600	
DB	541	AGCACAATATGACCTCCGCGCTGAAAGCCCGCTTGGAGACCTCTGAGACAGCTGTGAGCGG	600	
QY	601	CGGCGAGAGCGCGACCTTTCAGACGTGCGCTGTGATGATGCGGACAGAGGAACTGTCCG	660	
DB	601	CGGCGAGAGCGCGACCTTTCAGACGTGCGCTGTGATGATGCGGACAGAGGAACTGTCCG	660	
QY	661	CCTACTAGAGCGCTGCTGAGCTGTGTGCGACCCGAGAGGACATCTCTCGCCGTCTCAGAG	720	
DB	661	CCTACTAGAGCGCTGCTGAGCTGTGTGCGACCCGAGAGGACATCTCTCGCCGTCTCAGAG	720	
QY	721	TCTGTGAGCGCGGAAAGGTGTGCACTCCGAAAGGAGGACGTGCGCGCCGAGTGTGTC	780	
DB	721	TCTGTGAGCGCGGAAAGGTGTGCACTCCGAAAGGAGGACGTGCGCGCCGAGTGTGTC	780	
QY	781	GAAACCTAAACGAGCGCATTCGCGCGGAGCGTCAAGGCTCTACATCAGCTTCTGCGCTTGG	840	
DB	781	GAAACCTAAACGAGCGCATTCGCGCGGAGCGTCAAGGCTCTACATCAGCTTCTGCGCTTGG	840	
QY	841	GCGATGAGCTACCTTGGCTTCAAGATCTAGAGGTGCGCCCTTAGTGAATGAGGCTCGAGG	900	
DB	841	GCGATGAGCTACCTTGGCTTCAAGATCTAGAGGTGCGCCCTTAGTGAATGAGGCTCGAGG	900	
QY	901	GAGGCTTGTGCTGAGGAGCCCGAGAAATTGACCTCTGATTTTAAATTGAAATPAAGTGGG	960	
DB	901	GAGGCTTGTGCTGAGGAGCCCGAGAAATTGACCTCTGATTTTAAATTGAAATPAAGTGGG	960	
QY	961	GCTGGACACAAAAAATTTTTTTTTTAAAAA 989		

Db 961 GCTGGACACAAAAA 989

## RESULT 12

US-10-013-913A-305  
; Sequence 305, Application US/10013913A  
; Publication No. US20030083462A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Gurney, Austin J.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C40  
; CURRENT APPLICATION NUMBER: US/10/013,913A  
; PRIOR FILING DATE: 2002-07-15  
; PRIOR APPLICATION REMOVED - See File Wrapper or Palm  
; NUMBER OF SEQ ID NOS: 477  
; SEQ ID NO 305  
; LENGTH: 989  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-013-913A-305

Query Match 100.0%; Score 989; DB 14; Length 989;

Best Local Similarity 100.0%; Pred. No. 5.6e-226; Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCCCGGAGTCCGAGACTGTCCAGAGCTCCAGTCACTGACCTGTACTGCC 60  
Db 1 GCGGGCCCGGAGTCCGAGACTGTCCAGAGCTCCAGTCACTGACCTGTACTGCC 60  
QY 61 TCCCGCCGCTCTCCGCGCCGCGCATGACCAAGCCGCGCTCCGCTCCGCGCGCG 120  
Db 61 TCCCGCCGCTCTCCGCGCCGCGCATGACCAAGCCGCGCTCCGCTCCGCGCGCG 120  
QY 121 CGCTGGCCCTGCGCTCAGCCGCACTGAGGCGCGCTTCGCACTGGCTCTTCTG 180  
Db 121 CGCTGGCCCTGCGCTCAGCCGCACTGAGGCGCGCTTCGCACTGGCTCTTCTG 180  
QY 181 GCGCGTGCCTCCCATGCGGAGCGCGGAGAGAGAGTCTCTTCCCGGAGAGAGCC 240  
Db 181 GCGCGTGCCTCCCATGCGGAGCGCGGAGAGAGAGTCTCTTCCCGGAGAGAGCC 240  
QY 241 GCGTGTGAGATCTTCTGAGCCGCTCATGCGGAGAGAGCCGCGCTCGAAGCTGA 300  
Db 241 GCGTGTGAGATCTTCTGAGCCGCTCATGCGGAGAGAGCCGCGCTCGAAGCTGA 300  
QY 301 GCGTGTGAGCCCTGAGAGAGCGGAGGAGATTTCTATGATGACTGCGAGAGCCAGC 360  
Db 301 GCGTGTGAGCCCTGAGAGAGCGGAGGAGATTTCTATGATGACTGCGAGAGCCAGC 360  
QY 361 TCTTGGCCAACTGCGCGGCTCATTCAGGCGAAGAGGCGCTGGAACCTGAGACCTTCA 420  
Db 361 TCTTGGCCAACTGCGCGGCTCATTCAGGCGAAGAGGCGCTGGAACCTGAGACCTTCA 420  
QY 421 CGGGCTACTCGCCCTGCGCTTGGCCCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 480  
Db 421 CGGGCTACTCGCCCTGCGCTTGGCCCTTGGCGCTTGGCGCTTGGCGCTTGGCGCT 480  
QY 481 GCGAGTGAAGCGCGAGCGCCCGAGAGCTGAGAGCGGCGCTTGGAGGCAAGCGAGCGG 540

## RESULT 13

US-10-007-194A-305  
; Sequence 305, Application US/10007194A  
; Publication No. US20030092061A1  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Gurney, Austin J.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2830P1C6  
; CURRENT APPLICATION NUMBER: US/10/007,194A  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: 60/098716  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098723  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098749  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098750  
; PRIOR FILING DATE: 1998-09-01  
; PRIOR APPLICATION NUMBER: 60/098803  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098821  
; PRIOR FILING DATE: 1998-09-02  
; PRIOR APPLICATION NUMBER: 60/098843  
; PRIOR FILING DATE: 1998-09-02

Db 481 GCGAGTGAAGCGCGAGCCCGGAGCTGGAGCGGCCCTGTGAGGAGCGAGCGCG 540  
QY 541 AGCACAAGATGACCTCTCCGCTGAAAGCCCGCTTGGAGACCTTGGAGAGAGTGTGGGG 600  
Db 541 AGCACAAGATGACCTCTCCGCTGAAAGCCCGCTTGGAGACCTTGGAGAGAGTGTGGGG 600  
QY 601 CGGGGAGGCGCGGACCTTTCAGCGTGGCGCTGTGTGATGCGGAGAGAGAGTGTCTCG 660  
Db 601 CGGGGAGGCGCGGACCTTTCAGCGTGGCGCTGTGTGATGCGGAGAGAGAGTGTCTCG 660  
QY 661 CCTACTAGAGCGCTGCTGCAAGTCTGCTGCAAGCCCGAGAGGAGATCTCTGCTGAGAG 720  
Db 661 CCTACTAGAGCGCTGCTGCAAGTCTGCTGCAAGCCCGAGAGGAGATCTCTGCTGAGAG 720  
QY 721 TCTTGTGCGCGGAGAGTGTGCAAGTCTGCAAGCCCGAGAGGAGATCTCTGCTGAGAG 780  
Db 721 TCTTGTGCGCGGAGAGTGTGCAAGTCTGCAAGCCCGAGAGGAGATCTCTGCTGAGAG 780  
QY 781 GAAACCTAAGAGAGCATTCGCGCGGAGCGTCAAGGCTCAATCAAGCTCTCTGCTGAG 840  
Db 781 GAAACCTAAGAGAGCATTCGCGCGGAGCGTCAAGGCTCAATCAAGCTCTCTGCTGAG 840  
QY 841 GCGATGAGTCACTGAGCTTCAAGATCTGAGGCTGAGCCCTTACTGAGTGGCTCGAGG 900  
Db 841 GCGATGAGTCACTGAGCTTCAAGATCTGAGGCTGAGCCCTTACTGAGTGGCTCGAGG 900  
QY 901 GAGGTTGCTGCGGAGAGCCCGAGAGTTGACCTTGATTTTAAATCGAAATTAAGTGG 960  
Db 901 GAGGTTGCTGCGGAGAGCCCGAGAGTTGACCTTGATTTTAAATCGAAATTAAGTGG 960  
QY 961 GCTGGACACAAAAA 989  
Db 961 GCTGGACACAAAAA 989





Db	241	GCCTGTGGAGATATCTTCTGAGCCGCTCCATGCGGGAGCAACCGGCGCTGCGAAGCCTGA	300
Qy	301	GGCTGTGACCTCTGGAGCAGCCGCGAGGGGAGTTCTATGATGACTCTGGAGACAGAGCCAC	360
Db	301	GGCTGTGACCTCTGGAGCAGCCGCGAGGGGAGTTCTATGATGACTCTGGAGACAGAGCCAC	360
Qy	361	TCTTGGCCAACTCGGCGCGGCTCATCCAGAGCCAAAGAGCGCTGGAACCTGAGCACTTCA	420
Db	361	TCTTGGCCAACTCGGCGCGGCTCATCCAGAGCCAAAGAGCGCTGGAACCTGAGCACTTCA	420
Qy	421	CGGACTACTTCGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCT	480
Db	421	CGGACTACTTCGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCTTGCGCT	480
Qy	481	GGCAGGTGGACGCGCAGCCCCCGGAGCTGGAGCGGCCCCCTGTGGAGGCAAGCGAGCGG	540
Db	481	GGCAGGTGGACGCGCAGCCCCCGGAGCTGGAGCGGCCCCCTGTGGAGGCAAGCGAGCGG	540
Qy	541	AGCACAAGATCGACTTCGCGCTGAAAGCCCGCTTGAGAGCCCTGAGCGAGCTGCTGCGG	600
Db	541	AGCACAAGATCGACTTCGCGCTGAAAGCCCGCTTGAGAGCCCTGAGCGAGCTGCTGCGG	600
Qy	601	CGGCGCAGAGCGCGGCTTCTGACGTGGCGCTGGTGGATGGGAGCAAGAGACTGCTCGG	660
Db	601	CGGCGCAGAGCGCGGCTTCTGACGTGGCGCTGGTGGATGGGAGCAAGAGACTGCTCGG	660
Qy	661	CCTACTACGAGCGCTGCTGCGAGCTGCTGCGAGCCCGAGGAGTCTCGCGTCTCTCAGAG	720
Db	661	CCTACTACGAGCGCTGCTGCGAGCTGCTGCGAGCCCGAGGAGTCTCGCGTCTCTCAGAG	720
Qy	721	TCTGTGGCGCGGGGAGAGTGTGTCGAACTTCGAAAGGGGAGCTGTGGCGCGAGTGTGC	780
Db	721	TCTGTGGCGCGGGGAGAGTGTGTCGAACTTCGAAAGGGGAGCTGTGGCGCGAGTGTGC	780
Qy	781	GAAACCTTAAACGAAAGCATTCGCGCGGAGAGCTGAGGGTCTACATCAGCTCTGCGCTTG	840
Db	781	GAAACCTTAAACGAAAGCATTCGCGCGGAGAGCTGAGGGTCTACATCAGCTCTGCGCTTG	840
Qy	841	GCAGTGGACTCACCTTGCGCTTCAAGATCTAGGGCTGCGCCCTAGTGAATGTGGCTCAGG	900
Db	841	GCAGTGGACTCACCTTGCGCTTCAAGATCTAGGGCTGCGCCCTAGTGAATGTGGCTCAGG	900
Qy	901	GAGGTTGCTTGGGAAACCCGAGAAATGACCTTGAGTTTAAATTGAAATTAAGTGGG	960
Db	901	GAGGTTGCTTGGGAAACCCGAGAAATGACCTTGAGTTTAAATTGAAATTAAGTGGG	960
Qy	961	GCTGGAGACAAAAAAGAAAAAAGAAAAA 989	
Db	961	GCTGGAGACAAAAAAGAAAAAAGAAAAA 989	





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Db      481 GCGAGGTGACGCGCAGCCCCCGGAGCTGGGACGCCCCCTGTGAGGACAGCCGAGGCGG 540
Qy      541 AGCACAAGATGACCTCCGCGCTGAAGCCCGGCTTGAAGACCCTGAGCAGCTGTGTGGCGG 600
Db      541 AGCACAAGATGACCTCCGCGCTGAAGCCCGGCTTGAAGACCCTGAGCAGCTGTGTGGCGG 600
Qy      601 CGGCGAGAGCCGCGACCTTGCAGCGTGGCCGTGTGATGCGGACAGAGAACTGTCTCG 660
Db      601 CGGCGAGAGCCGCGACCTTGCAGCGTGGCCGTGTGATGCGGACAGAGAACTGTCTCG 660
Qy      661 CCTACTACGAGGCTGCGCTGAGAGCTGTGAGACCCGAGAGGATCTGCGCGCTCTAGAG 720
Db      661 CCTACTACGAGGCTGCGCTGAGAGCTGTGAGACCCGAGAGGATCTGCGCGCTCTCTAGAG 720
Qy      721 TCTGTGCGCGGGAAGGTGTGTGCAACCTCGAAAGGGAAGGTGGCGGCGCGAGTGTGTG 780
Db      721 TCTGTGCGCGGGAAGGTGTGTGCAACCTCGAAAGGGAAGGTGGCGGCGCGAGTGTGTG 780
Qy      781 GAAACCTTAAAGAGAGGATCGGCGGAGCGTCAAGGTCCTACATCAGGCTCTGCCCCCTG 840
Db      781 GAAACCTTAAAGAGAGGATCGGCGGAGCGTCAAGGTCCTACATCAGGCTCTGCCCCCTG 840
Qy      841 GCGATGGACTGACCTTGGCTTCAAGATCTAGGCTGAGCCCTAGTGAAGTGGCTCGAGG 900
Db      841 GCGATGGACTGACCTTGGCTTCAAGATCTAGGCTGAGCCCTAGTGAAGTGGCTCGAGG 900
Qy      901 GAGGTTGGCTTGGGAACCCGAGAAATGACCCCTGAGTTTAAATTGAAAAATAAGTGG 960
Db      901 GAGGTTGGCTTGGGAACCCGAGAAATGACCCCTGAGTTTAAATTGAAAAATAAGTGG 960
Qy      961 GCTGGGACACAAAAAAGAAAAAAGAAAAA 989
Db      961 GCTGGGACACAAAAAAGAAAAAAGAAAAA 989
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Search completed: April 10, 2004, 16:26:03  
Job time : 415 secs



Qy	59	CTGAGCGCGCGGACGCGGCACCTTCGACCTGGCGGTGGTATGCGGCAAGAGAAAC	653
Db	568	CTGACCAAGGCGCTGGCGCGGCGAGTTTCGACTCGGCTTCATCGACGCGCAAGAGCCAAAC	627
Qy	654	TGCGCGCGCTACTACGAGGCGTGCCTGACGTCGTCGCGAACCCGAGAGGATCCTGCGGTC	713
Db	628	TACCCGAAATACCTGGAAGCGCGCGCTGGCGCTGGTGGCGCAAGGTGGGCTGGTCTTTC	687
Qy	714	CTCGAATCTCTGTCGCGCGCGGAAAGTGGCTGCACCTCGGAAAGGAGACGTGGCGCGGAG	773
Db	688	GACACCTGCTGTGGAGCGGCGCGGGTCTCTGAAGCGGACCCGAAAGATGGCGATACCCGC	747
Qy	774	TGTGTGGAAACTAAACGAGCGATCCGCGCGGACGTCAGGGCTTAATATAGCTCTTG	833
Db	748	GGCATCCAGCAGCTCAACTGGCGCTGAAAGAACGAGCGCGGGTGGACTTACTCGTGTG	807
Qy	834	CCCTGGCGCATGAGACTCACCTTGGGCTTCAAGATCT	870
Db	808	CCGATCGGCGACGGGCTGAGCGGTCTGTGCGCAAGCGCT	844

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RESULT 2
US-09-452-239-45
, Sequence 45, Application US/09452239
, Patent No. 6465229
, GENERAL INFORMATION:
, APPLICANT: Rafalski, Antoni J.
, APPLICANT: Pader, Gary M.
, APPLICANT: Cahoon, Rebecca E.
, TITLE OF INVENTION: Plant Caffeoyl-CCA O-Methyltransferase
, FILE REFERENCE: BR184 US NA
, CURRENT APPLICATION NUMBER: US/09/452,239
, CURRENT FILING DATE: 1999-12-01
, EARLIER APPLICATION NUMBER: 60/110,594
, EARLIER FILING DATE: 1998-December-02
, NUMBER OF SEQ ID NOS: 50
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 45
, LENGTH: 953
, TYPE: DNA
, ORGANISM: Triticum aestivum
US-09-452-239-45

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Query Match	16.4%;	Score 161.8;	DB 4;	Length 953;
Best Local Similarity	55.1%;	Pred. No. 1.5e-22;		
Matches 338;	Conservative	0;	Mismatches 272;	Indels 3; Gaps 1.

QY 273 CGGAGAGACCCGGGCGCTGGCCAAAGCCTTGAGGCTCTGTACACCTTGAGACACACCCGAGGGAGAT 332  
 Db 186 CGCGAGACGAGATGACATCGCGGACCTGCGCTCATATACCGAAGAACACCCATGGGGTTAC 245  
 QY 333 TCTATGATGACCTGCGAGCAGGCCACCTTTGGCCAACTGGACCGGCTCATATCCAGGC 392  
 Db 246 ATGCAGTCGTCTCTGGAGCAGGCGGACGTGCTGGGAGTGTATCAAGATGGCGGGCGCC 305  
 QY 333 AAGAAGGCGCTGGACCTGGGACACCTTCAAGGGTATCTCGGCCCTGGCCCTGGCG 455  
 Db 306 AAGAAGAGATCGAGGTGGGCGTGTTCACGGGTACTCTGTGTGGCACCAGCTGGCG 365  
 QY 453 CTGACCGCGGACGAGGCGCCTGATGACCTGTGAGATGAGACGCGACCCCGGAGCTGGGA 512  
 Db 366 CTCCCGGAGGACGGGCAAAGTGTGGCCATGACACCGACCGGAGTGTACGAGGTGGGT 425  
 QY 513 CGGCCCTGTGTGAAGCAGGCGCGAAGCGGAGACAAATGACCTTCGGCTGAAGCCGCC 572  
 Db 426 CGCCCTTCATCGAAGGCGCGGATGGCCCAAGTGTGAATCTTCGCGAGGGACACCGGC 485  
 QY 573 TTGAGACCTCGGACGAGGCTGTGGCGCGGGGCGA---GAGCGGACCTTGCAGCTGGCC 625  
 Db 486 CTGGGCGCCCTGGAGGAGTCTCTGTGTGAAGAGACGAGCGCGGAGGCTACGACCTTGGCG 545  
 QY 630 GTGTGATGCGGACCAAGAGAACTGCTCGCCTTACTAGAGGCGTGTGCACTGTGCTG 685

Db	546	TTGTGGAAGCGGACAAAGCCAACTACCTGCGCTACCAACGACGAGCTGTGAAGCTGGTC	603
Qy	690	CGACCCGGAAGGATCCTCGCCGCTCTTCAAGTCCCTGTGGCGCGGGAAGATGTGCAACT	749
Db	606	CGGCTGCGCGGACATATCTATCAACAACAACGCTCTGCGGCGGCAAGGTGGCCCTCCG	665
Qy	750	CCGAAAGGGGACGTGGCGGCGCGAGTGTGTGCAAACTTAAAGAACGATCCGGCGGAC	809
Db	666	GCGGAGACCCCATGTGCGACCTCGACACCGGCTTCTCCGCGGCTCAGGGAACCTCAAC	725
Qy	810	GTTAGGGTTAATCAATCAGCCTCTCTGGCCCTGGGCGATGATCTCAACTTGGCTTCAATC	869
Db	726	GCCAACTCGCGGCCAACCCCGGATCGAAGGTGTGCCAGCTCGCCATCGCGACGAGTTC	785
Qy	870	TAGGGCTGGCCCC	882
Db	786	ACCATCTGCCGCC	798

```

, RESULT 3
, US-09-452-239-43
, Sequence 43, Application US/09452239
, Patent No. 6465229
, GENERAL INFORMATION:
, APPLICANT: Katalerki, Antoni J.
, APPLICANT: Fader, Gary M.
, APPLICANT: Canoon, Rebecca E.
, TITLE OF INVENTION: Plant Caffecyl-CoA O-Methyltransferases
, FILE REFERENCE: B8184 US NA
, CURRENT APPLICATION NUMBER: US/09/452,239
, CURRENT FILING DATE: 1999-12-01
, EARLIER APPLICATION NUMBER: 60/110,594
, EARLIER FILING DATE: 1998-December-02
, NUMBER OF SEQ. ID NOS: 50
, SOFTWARE: Microsoft Office 97
, SEQ ID NO 43
, LENGTH: 1049

```

```

? ORGANISM: Triticum aestivum
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (352)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (948)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (992)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (994)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (999)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (1003)
? FEATURE:
? NAME/KEY: unsure
? LOCATION: (1038)
US-09-452-239-43

```

Query Match	16.1%;	Score 159.2;	DB 4;	Length 1049;
Best Local Similarity	54.8%;	Pred. NO. 4.7e-22;		
Matches 336;	Conservative	0;	Mismatches 274;	Indels 3;
				Gaps 1.

QY 273 GGGAGACACCCGGGGCTCCAAAGCTTAGAGGCTGACCCCTGAGACACCCGACGGGGAT 332  
Db 186 CCGGACGACGAGTGAATGCGGACCTGGGCTCATACGACAGACACCCATGGGGTTAC 245  
QY 333 TCTATGATGACTCTGGAGACAGGCCCACTCTTGGCCAACTGGGGCGGCTCATCCAGGC 392  
Db 246 ATGCACTGCTCTTCGACACAGGCGGAGCTGCTGGGGATGCTGATCAAGATGGCGGGCCG 305

QY 393 AAGAGGCGCTGAGACCTTGAACGGGCTACTCCGCTGAGCCCTTGGCCCTTGGCG 452  
 Db 306 AAGAGAGCATGAGAGTGGGCTGTTCACGGGCTACTCGCTGCTGAGCACCGGCTGGCG 365  
 QY 453 CTGCCCCGAGACGGGCGGCTGTGTACTGAGAGGTGAGACGGCCCGGAGCTGGGA 512  
 Db 366 CTCCCGAGAGACGGGAGTGTGTGGGATGACACCGACCGAGTGTCTACGAGTGGGT 425  
 QY 513 CGGCCCCCTGTGAGAGGAGCGAGCGGAGAGCAAGATCGACTCCGGCTGAAAGCCGCG 572  
 Db 426 CGCCCTTTCATTGAGAGAGCGGCGGATGAGCGGACAAAGGTGACTTCCCGAGAGGACCGCG 485  
 QY 573 TTGAGACCTTGAACGAGCTGTGCGCGCGGCGGA--GGCGGACCTTTCAGAGTGGCC 629  
 Db 486 CTGGCGGCGCTGAGACGAGCTCTCTGTCAGAGAGCGACGCGCGGCGAGCTACGACTTGGCG 545  
 QY 630 GTGGTGAATGCGGCAAGAGAGACTGCTCCGCTTACTACAGAGCGCTGCTGACGCTGCTG 689  
 Db 546 TTCTGTGACGCGACAAAGCCCACTTACGTGCGCTTACACAGAGAGCTGTGAAAGCTGGTC 605  
 QY 690 CGACCCGAGAGCATCTCGCCGCTCTGAGTCTGTGCGCGGAGAGTGTCTGCAACT 749  
 Db 606 CGCGTCGGCGGACATCATCTATGACAAACGCTCTGGGGCGGCAAGTGGGCGCTGGCG 665  
 QY 750 CCGAAAGGGAGCTGGGCGGCGGAGTGTGTGGAACCTTAAAGAGCATCCGGCGGAG 809  
 Db 666 GCGGAGCAACCCCATGTCTGACCTGAGACCCGCTTCCGCGCGCTCAGAGACTTCAC 725  
 QY 810 GTCAAGGCTCTACATCAAGCTCTCTGCGGCGGATGAGACTCACTTGGCTTCAAGATC 869  
 Db 726 GCCAAGCTCGCGCGCGAGCCCGGATGAGAGTCTGCCAGCTCGGCAATCGCGAGCGTC 785  
 QY 870 TAGGCGTGGCCCC 882  
 Db 786 ACCATCTGCGCGC 798

RESULT 4  
 US-09-452-239-13  
 ; Sequence 13, Application US/09452239  
 ; Patent No. 6465229  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni J.  
 ; APPLICANT: Fader, Gary M.  
 ; APPLICANT: Cahoon, Rebecca E.  
 ; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase  
 ; FILE REFERENCE: B01284 US NA  
 ; CURRENT APPLICATION NUMBER: US/09/452,239  
 ; EARLIER FILING DATE: 1999-12-01  
 ; EARLIER APPLICATION NUMBER: 60/110,594  
 ; EARLIER FILING DATE: 1998-December-02  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 13  
 ; LENGTH: 997  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; NAME/KEY: unsure  
 ; LOCATION: (483)  
 US-09-452-239-13

Query Match 16.0%; Score 158.6; DB 4; Length 997;  
 Best Local Similarity 54.2%; Pred. No. 6,1e-22;  
 Matches 373; Conservative 0; Mismatches 300; Indels 15; Gaps 2;

QY 273 CGGAGAGACCGGCGGCTGCGAAGCTTGAAGCTGTGACCTTGAAGAGCGCGGAGGAGAT 332  
 Db 187 CGGAGAGCGGAGTGCATGCGGATTCGCGCTTATCAGAGCAAGACCAAGGAGGATTC 246  
 QY 333 TCTATGATGACCTCGAGACGCGCCAGCTCTTGGCCCAACTGCGCGGCTCATTCAGGCC 392

Db 247 ATGCAATGCTCGGCGGATGAGCGGAGCTGTGGGAGATCTGCTGAGATGAGCCGAGCG 306  
 QY 393 AAGAGGCGCTGAGACCTTGGAGACCTTCAAGGCTTACTCGGCTTGGCCCTTGGCG 452  
 Db 307 AAGAGAGCATGAGAGTGGGCTGTTCACGGGCTACTCGCTGCTGAGCACCGGCTGGCG 366  
 QY 453 CTGCCCCGAGACGGGCGGCTGTGTACTGAGAGGTGAGACGGCCCGGAGCTGGGA 512  
 Db 367 CTCCCGAGAGACGGGAGTGTGTGGGATGACACCGGACAGGAGAGCTTACGAGTCCGG 426  
 QY 513 CGGCCCCCTGTGAGAGGAGCGGCGGAGAGCAAGATCGACTCCGGCTGAAAGCCGCG 572  
 Db 427 CGGCGCTTCTTGAAGAGCGGCGGATGAGCGGACAAAGTGTGACTTCCAAAGGAGAAAGG 486  
 QY 573 TTGAGACCTTGAACGAGCTGCT-----GGCGGCGGCGAGGCGGCACTTTC 620  
 Db 487 CTGAGAGAGCTGAGAGAGCTGCTCGCGAGAGGCGGCGGCGGCGGCGGCGGCTTC 546  
 QY 621 GACGTGGCGCTGTGATGAGTGCAGAGAGAACTGCTCGGCTTACTACAGAGCTGGCTG 680  
 Db 547 GACTTCGGGCTGTGAGACGCGGACAAAGCCCACTACGTCAAGTACACAGAGAGCTGCTG 606  
 QY 681 CAGCTGTGCGACCGGAGGAGCATCTCGCCGCTCTCAAGTCTGTGCGCGGAGAGTGTG 740  
 Db 607 CAGCTGTGCGGCTGTGCGGCGGAGCATCTGTGACAAACGCTGTGGGCGGCGGAGTGTG 666  
 QY 741 CTGCAACTCCGAAAGGGAGCTGGCGGCGGAGTGTGTGGAACCTTAAAGAGCATC 800  
 Db 667 GCGCTGCGCGCGGAGACCGGCTGTGAGACCTGAGACCGGAGTGTCTCGGCGCATCGG 726  
 QY 801 CGGCGGAGAGTGAAGGTCTACATGAGCTCTCGGCGGATGAGTCACTTGGCC 860  
 Db 727 GACTTCACTCGAGGCTGCGGCGGAGCCCGGATGAGAGTCTGCAACTTGGCATTCGCC 786  
 QY 861 TTCAAGAT--CTAAGGCTGGGCGGCTTGTGAGTGGGCTGAGAGAGGCTTGGGAGAC 917  
 Db 787 GACGGATTCACATCTGCGCGGCTCTGTGAGGTGTCAGACCGGAGCTTACCGGCGGA 846  
 QY 918 CCCAGAGATGAGCCCTGAGGTTTAAT 945  
 Db 847 TCCATTCATCGCTCTCGCGTGAATTAAT 874

RESULT 5  
 US-09-452-239-41  
 ; Sequence 41, Application US/09452239  
 ; Patent No. 6465229  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rafalski, Antoni J.  
 ; APPLICANT: Fader, Gary M.  
 ; APPLICANT: Cahoon, Rebecca E.  
 ; TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase  
 ; FILE REFERENCE: B01284 US NA  
 ; CURRENT APPLICATION NUMBER: US/09/452,239  
 ; EARLIER FILING DATE: 1999-12-01  
 ; EARLIER APPLICATION NUMBER: 60/110,594  
 ; EARLIER FILING DATE: 1998-December-02  
 ; NUMBER OF SEQ ID NOS: 50  
 ; SOFTWARE: Microsoft Office 97  
 ; SEQ ID NO 41  
 ; LENGTH: 1078  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum  
 US-09-452-239-41

Query Match 15.9%; Score 157.2; DB 4; Length 1078;  
 Best Local Similarity 57.1%; Pred. No. 1,1e-21;  
 Matches 307; Conservative 0; Mismatches 228; Indels 3; Gaps 1;

QY 214 AGTGCCTGCTTCCCCCGAGAGAGCGGCTGTGAGAGTATCTTGAAGCGGCTTCATGC 273  
 Db 200 AAGAGCTGTCTCAGAGAGCAGCCCTCTTACAGTACATCTGAGAGAGAGCGGTGTACCCGC 259

```

QY 274 GGGAGACCCGCGCTGCGAAGCCTTGAGCTGTGACCTTGAGACCGCGAGGGGANTT 333
DB 260 GCGAGCAGATGATCATTAAGAGAGCTCCGCGAGATCAACCGCAACCGCATGGAACCTGA 319
QY 334 CTATGATGACCTGCGAGACGAGCCCAAGCTTTGGCCAACTGCGCGGCTCATTCAGGCCA 393
DB 320 TGACGAGCTGCGGCGAGACGAGGCGCAATTCCTCAACATGCTGCTCAAGCTCATGCGGCCA 379
QY 394 AGAAGCGCTGGAACCTTGCGCACTTCAAGGCTTCCGCTTGCGCTTGCGCTTGCGCC 453
DB 380 AGAAGACCATGAGATGCGCGCTTCAACCGCTTACCTCCCTCGCGCACCGCGCTGCGCA 439
QY 454 TGCGCGGAGACGCGCGCTGCTGATGACCTGAGAGGAGCGCGACCGCGCGAGCTGAGAC 513
DB 440 TCCCGAGACGAGCAGCATCTTGCGCATGACATCAACCGCGAAGAACTACGAGCTGAGGC 499
QY 514 GAGCCCTGTGAGAGCAGCGCGAGCGAGCAAGATGACCTTCGCGCTGGAAGCCCGCT 573
DB 500 TGCGGTGATGAGAGAGCGCGCGCTGCGCAAGATGACCTTCGCGAGAGCGCGCGCG 559
QY 574 TGAAGACCTGAGACGAGCTGTGCGCGC---GGCGAGCGCGGACCTTGAGAGCTGCG 630
DB 560 TGCGGTGCTGAGAGCGCGCTGCTGAGAGCAGAGCGCAACAGCGACCTTGAGCTGCT 619
QY 631 TGTGATGCGGAGCAAGAGAACTGCTCCGCTACTACGAGCGCTGCGCTGAGCTGCTGC 690
DB 620 TGTGAGAGCGCGAGCAAGAGCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 679
QY 691 GACCGGAGGAGCTCTGCGCGCTCTCAAGATCTCTGCGCGCGAGAGGCTGCAACC 748
DB 680 AGTCGCGCGCGCTCTCTGCGCTACGACAGACGCTCTGGAAGCGCTCTCGTGTCTCC 737

```

```

RESULT 6
US-09-452-239-35
; Sequence 35, Application US/09452239
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffey1-CoA O-Methyltransferase
; FILE REFERENCE: B01284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 1018
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE:
; LOCATION: (817)
; NAME/KEY: unsure
; FEATURE:
; LOCATION: (826)
; NAME/KEY: unsure
; FEATURE:
; LOCATION: (874)
; NAME/KEY: unsure
; LOCATION: (891)
; NAME/KEY: unsure
; FEATURE:
; LOCATION: (924)
; NAME/KEY: unsure
; LOCATION: (934)
; FEATURE:
; NAME/KEY: unsure

```

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; LOCATION: (961)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (970)..(971)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1012)
US-09-452-239-35

```

```

Query Match
Best Local Similarity 56.6%; Pred. No. 2.3e-21;
Matches 309; Conservative 0; Mismatches 234; Indels 3; Gaps 1;

```

```

QY 214 AGTCGCTGCTTCCCCGAGAGACGCGCGCTGTGACAGTATCTTCTGAGCGCTGCATGC 273
DB 177 AGAGCTTCTCAAGAGCAAGACGACCTGTACAGTACATCTGTGACACGAGCGCTGTACCGCG 236
QY 274 GCGAGCACCGCGCGCTGCGAAGCTTGAAGCTGTGACCTTGAGACAGCGCGAGGGGATTT 333
DB 237 GCGAGCCGAGAGCATGAAAGAGCTGCGCGAGATCACCGCAACACCATGGAACCTGA 296
QY 334 CTATGATGACCTGAGAGAGCGCGAGCTTGGCAACTGCGCAACTGCGCGGCTCATCCAGGCCA 393
DB 297 TGACCATCTCGCGAGCAGAGGCGCAATCTTCAACATGCTCATAGCTCATTCGCGGCCA 356
QY 394 AGAAGCGCTGAGACCTGCGGCACTTCAAGGCTTACCTCGCGCTGAGCGCTTGCGCGC 453
DB 357 AGAAGACCATGAGAGTGGCGGTATACCGGCTACTCCCTGCTGCGCACCGCGCTCGCCA 416
QY 454 TGCGCGGAGAGCGCGCGCTGTGATGACCTGAGAGTGAAGAGCGACCGCGAGAGCTGAGAC 513
DB 417 TCCCGAGAGCGGACCATCTTGGCATGACATCAACCGGAGAACTACAGAGCTTGGGCG 476
QY 514 GAGCCCTGTGAGAGCGCGAGCGAGCGAGCAAGATGACCTTCGCGCTGGAAGCCCGCT 573
DB 477 TGCGGTGATGAGAGAGCGCGCGCGCTGCGCAAGATGACCTTCGCGAGAGCGCGCGCG 536
QY 574 TGAAGACCTGAGACGAGCTGTGCGCGC---GGCGAGCGCGGACCTTGAGAGCTGCG 630
DB 537 TGCGGTGCTGAGAGCGCGCTGCTGAGAGCAGAGCGCAACAGCGGACCTTGAGCTGCT 596
QY 631 TGTGATGCGGAGCAAGAGAACTGCTCCGCTACTACGAGCGCTGCGCTGAGCTGCTGC 690
DB 597 TGTGAGAGCGCGAGCAAGAGCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 656
QY 691 GACCGGAGGAGCTCTGCGCGCTCTCAAGATCTCTGAGAGTGTGCGCGGAGAGTGTGCACTTC 750
DB 657 AGTCGCGCGCGCTCTCGGCTACGACAGACCTCTGGAAGCGCTCTCGTGTCTCCGCG 716
QY 751 CGAAG 756
DB 717 CGAGG 722

```

```

RESULT 7
US-09-452-239-1
; Sequence 1, Application US/09452239
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni J.
; APPLICANT: Fader, Gary M.
; APPLICANT: Cahoon, Rebecca E.
; TITLE OF INVENTION: Plant Caffey1-CoA O-Methyltransferase
; FILE REFERENCE: B01284 US NA
; CURRENT APPLICATION NUMBER: US/09/452,239
; EARLIER FILING DATE: 1999-12-01
; EARLIER APPLICATION NUMBER: 60/110,594
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 1
; LENGTH: 891
; TYPE: DNA

```

ORGANISM: Zea mays  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (806)  
FEATURE:  
NAME/KEY: unsure  
LOCATION: (810)  
US-09-452-239-1

Query Match 15.6%; Score 154; DB 4; Length 891;  
Best Local Similarity 56.7%; Pred. No. 4, 5e-21;  
Matches 305; Conservative 0; Mismatches 230; Indels 3; Gaps 1;

QY 214 AGTCCCTGCTCCCGGAGAGACAGCCGCTGTGGGAGTATCTTCTGAGCGGCTCATC 273  
DB 181 AGAGCTGCTCAAG 240  
QY 274 GGGAGACCCGCGCGCTGCGAAAGCTGAGGCTGCTGAGAGAGAGAGAGAGAGAG 333  
DB 241 GGGAGCGGAG 300  
QY 334 CTATGATGACCTGGGAG 393  
DB 301 TGAAGACCTCGGCTGAG 360  
QY 394 AGAAGCGCTGAGACCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 453  
DB 361 AGAAGACATGAG 420  
QY 454 TGCCCGGAG 513  
DB 421 TCCGAG 480  
QY 514 GAGCCCTGAG 573  
DB 481 TTCCCTGATCAAG 540  
QY 574 TGAAGACCTGAG 630  
DB 541 TCCCGCTGAG 600  
QY 631 TGGGATGAG 690  
DB 601 TGGGATGAG 660  
QY 691 GAGCCGAG 748  
DB 661 GAGCCGAG 718

## RESULT 8

US-09-410-551B-1  
Sequence 1, Application US/09410551B  
Patent No. 6503737  
GENERAL INFORMATION:  
APPLICANT: KOSAN BIOSCIENCES, Inc.  
APPLICANT: REEVES, CHRISTOPHER  
APPLICANT: CHU, DANIEL  
APPLICANT: KHOSLA, CHAITAN  
APPLICANT: SANI, DANIEL  
APPLICANT: WU, KAI  
TITLE OF INVENTION: POLYKETIDE SYNTHASE ENZYMES AND RECOMBINANT DNA  
FILE REFERENCE: 30062-20026.00  
CURRENT FILING DATE: 1999-10-01  
PRIOR FILING DATE: 1999-06-17  
PRIOR APPLICATION NUMBER: US 60/139,650  
PRIOR FILING DATE: 1999-03-11  
PRIOR APPLICATION NUMBER: US 60/123,810  
PRIOR FILING DATE: 1998-10-02  
PRIOR APPLICATION NUMBER: US 60/102,748  
NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1  
LENGTH: 77536  
TYPE: DNA  
ORGANISM: Streptomyces hygroscopicus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (52275)...(71465)  
US-09-410-551B-1

Query Match 15.5%; Score 153; DB 4; Length 77536;  
Best Local Similarity 55.4%; Pred. No. 1, 2e-20;  
Matches 341; Conservative 0; Mismatches 265; Indels 9; Gaps 2;

QY 252 TATCTTGAAGCGGCTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311  
DB 8195 TACGATGAG 8254  
QY 312 CTGAG 368  
DB 8255 GCGAG 8314  
QY 369 AACCTGAG 428  
DB 8315 TTCTGAG 8374  
QY 429 TCCGCTGAG 488  
DB 8375 AGCAG 8434  
QY 489 GAGCGAG 548  
DB 8435 ATGCGAG 8494  
QY 549 ATGAG 602  
DB 8495 ATGAG 8554  
QY 603 GAGCGAG 662  
DB 8555 GCGAG 8614  
QY 663 TACTGAG 722  
DB 8615 TACTGAG 8674  
QY 723 CTGAG 782  
DB 8675 CTGAG 8734  
QY 783 AACCTAAG 842  
DB 8735 GAGCTAAG 8794  
QY 843 GATGAG 857  
DB 8795 GAGCGAG 8809

## RESULT 9

US-09-452-239-37  
Sequence 37, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Rafalski, Antoni J.  
APPLICANT: Fader, Gary M.  
APPLICANT: Cahoon, Rebecca E.  
TITLE OF INVENTION: Plant Caffeoyl-CoA O-Methyltransferase  
FILE REFERENCE: BB1284 US NA  
CURRENT FILING DATE: 1999-12-01  
PRIOR FILING DATE: 1999-12-01  
PRIOR APPLICATION NUMBER: US/09/452,239  
PRIOR FILING DATE: 1998-December-02  
PRIOR APPLICATION NUMBER: 60/110,594

NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 37  
LENGTH: 1118  
TYPE: DNA  
ORGANISM: Triticum aestivum  
US-09-452-239-37

Query Match 15.0%; Score 148; DB 4; Length 1118;  
Best Local Similarity 53.7%; Pred. No. 6.4e-20;  
Matches 366; Conservative 0; Mismatches 295; Indels 21; Gaps 2;

214 AGTGCCTGCTTCCCCCGAGAGACAGCCCGCTGTGGAGTATCTTGTAGCCGCTCATGC 273  
184 AGAGCTGCTCAAGAGCAGACCTTACACAGTATCTTGTAGACAGAGCTTACCCG 243  
274 GGGAGCACCAGCGCTGCGAAGCTGAGGCTGTGACCTGTGAGCAGCCGAGGGGATT 333  
244 GGGAGCCGAGAGCATGAGAGCTCCGCGAGATCACCGCCAGCACTGAGACCTGA 303  
334 CTATGATGACTGTGAGAGAGCCGACCTTGTGCGACACCTGGCGGCTCATCCAGGCCA 393  
304 TGACACCTCGCGCGAGCAGAGGCGAGTCTTGAACATGCTCATGAGCTCATCGCGCCA 363  
394 AGAAGCGCTGAGACCTGTGGACCTTCAAGGCTTACTCCGCTGTGACCTGTGCGC 453  
364 AGAAGACCATGAGATGCGCGCTTACACCGGCTTCTCCCTCTCGCCAGCGCGCTGCCC 423  
454 TGCCCGCGAGCGCGCGCTGTGATCTGCGAGGTGAGACGCGACCCCGAGCTGGAC 513  
424 TCCCGAGAGAGCGCAGATCTTGGCCATGACATCAACCGGAGAACTTACAGCTGGCC 483  
514 GGCCCTGTGAGAGCGAGCGCGAGCGAGCAAGATGACCTCCGCTGAAGCCGCT 573  
484 TGCCCTGATGAGAAAGCCGCGCTGCGCCACAGATGACTTCCGAGAGGTCCCGCG 543  
574 TGGAGACCTTGAGACGAGTGTGCGCGCGCGAG--GCCGACCTTGTGACCTGGCG 630  
544 TCCCGCTCTGAGACGACTTCTGCGGAGAGAAAGAACAGGGTCTTCACTTCTCT 603  
631 TGTGTGATGCGGAGCAAGAGAACTGCTCGGCTTACTAGAGCGGTGAGCTGTGCG 690  
604 TGTGTGAGCGCGAGCAAGAACTTACTTCACTTACACGAGCGGTGTGAGTGTGA 663  
691 GACCCGAGAGCATCTTCCGCTCTCAAGATCTGTGCGCGGAGAGGTGTGACCTTC 750  
664 AGCTGGCGGCTCTCATCGGCTTACGACAAACGCTGTGAGACGGCTCGTCTCCCG 723  
751 CGAAAGGAGACGTGGCGGC-----CGAGTGTGTGGAACCTTAAAG 792  
724 AGCAGCGCGCCATGCGCAAGTACATCGCTTCTACCGGACCTGTGTCTCTCAACA 783  
793 AACGATCCGCGGAGAGCTCAAGGTTCTATCATGAGCTTCTGCGCTGGCGATGACTCA 852  
764 AGCGCTCGCGCGCGAGCAGCGCGCTGAGATGTGCACTCCCGTGGCGACGCGCTCA 843  
853 CTTGGCCTTCAAGATCTTAGG 874  
844 CCTCTGCGCGCGCTCAAGTG 865

RESULT 10  
US-09-452-239-3  
Sequence 3, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Rafaleksi, Antoni J.  
APPLICANT: Fader, Gary M.  
APPLICANT: Cahoon, Rebecca E.  
TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase  
FILE REFERENCE: B1284 US NA  
CURRENT APPLICATION NUMBER: US/09/452,239  
CURRENT FILING DATE: 1999-12-01

EARLIER APPLICATION NUMBER: 60/110,594  
EARLIER FILING DATE: 1998-December-02  
NUMBER OF SEQ ID NOS: 50  
SOFTWARE: Microsoft Office 97  
SEQ ID NO: 3  
LENGTH: 1146  
TYPE: DNA  
ORGANISM: Zea mays  
US-09-452-239-3

Query Match 15.0%; Score 148; DB 4; Length 1146;  
Best Local Similarity 53.7%; Pred. No. 6.5e-20;  
Matches 366; Conservative 0; Mismatches 295; Indels 21; Gaps 2;

214 AGTGCCTGCTTCCCCCGAGAGACAGCCCGCTGTGGAGTATCTTGTAGCCGCTCATGC 273  
189 AGAGCTGCTCAAGAGCAGACCTTACACAGTATCTTGTAGACAGAGCTTACCCG 248  
274 GGGAGCACCAGCGCTGCGAAGCTGAGGCTGTGACCTGTGAGCAGCCGAGGGGATT 333  
249 GGGAGCCGAGAGCATGAGAGCTCCGCGAGATCACCGCCAGCACTGAGACCTGA 308  
334 CTATGATGACTGTGAGAGAGCCGACCTTGTGCGACACCTGGCGGCTCATCCAGGCCA 393  
309 TGACACCTCGCGCGAGCAGAGGCGAGTCTTGAACATGCTCATGAGCTCATCGCGCCA 368  
394 AGAAGCGCTGAGACCTGTGGACCTTCAAGGCTTACTCCGCTGTGACCTGTGCGC 453  
369 AGAAGACCATGAGATGCGCGCTTACACCGGCTTCTCCCTCTCGCCAGCGCGCTGCCC 428  
454 TGCCCGCGAGCGCGCGCTGTGATCTGCGAGGTGAGACGCGACCCCGAGCTGGAC 513  
429 TCCCGAGAGAGCGCAGATCTTGGCCATGAGATCAACCGGAGAACTTACAGCTGGCC 488  
514 GGCCCTGTGAGAGCGAGCGCGAGCGAGCAAGATGACCTCCGCTGAAGCCGCT 573  
489 TGCCCTGATGAGAAAGCCGCGCTGCGCCACAGATGACTTCCGAGAGGTCCCGCG 548  
574 TGGAGACCTTGAGACGAGTGTGCGCGCGCGAG--GCCGACCTTGTGACCTGGCG 630  
549 TCCCGCTCTGAGACGACTTCTGCGGAGAGAAAGAACAGGGTCTTCACTTCTCT 608  
631 TGTGTGATGCGGAGCAAGAGAACTGCTCGGCTTACTAGAGCGGTGAGCTGTGCG 690  
609 TGTGTGAGCGCGAGCAAGAACTTACTTCACTTACACGAGCGGTGTGAGTGTGA 668  
691 GACCCGAGAGCATCTTCCGCTCTCAAGATCTGTGCGCGGAGAGGTGTGACCTTC 750  
669 AGCTGGCGGCTCTCATCGGCTTACGACAAACGCTGTGAGACGGCTCGTCTCCCG 728  
751 CGAAAGGAGACGTGGCGGC-----CGAGTGTGTGGAACCTTAAAG 792  
729 AGCAGCGCGCCATGCGCAAGTACATCGCTTCTACCGGACCTGTGTCTCTCAACA 788  
793 AACGATCCGCGGAGAGCTCAAGGTTCTATCATGAGCTTCTGCGCTGGCGATGACTCA 852  
789 AGCGCTCGCGCGCGAGCAGCGCGCTGAGATGTGCAAGTCCCGTGGCGACGCGCTCA 848  
853 CTTGGCCTTCAAGATCTTAGG 874  
849 CCTCTGCGCGCGCTCAAGTG 870

RESULT 11  
US-09-452-239-5  
Sequence 5, Application US/09452239  
Patent No. 6465229  
GENERAL INFORMATION:  
APPLICANT: Rafaleksi, Antoni J.  
APPLICANT: Fader, Gary M.  
APPLICANT: Cahoon, Rebecca E.  
TITLE OF INVENTION: Plant Caffeyol-CoA O-Methyltransferase  
FILE REFERENCE: B1284 US NA





```

CURRENT APPLICATION NUMBER: US/09/452,239
CURRENT FILING DATE: 1999-12-01
EARLIER APPLICATION NUMBER: 60/110,594
EARLIER FILING DATE: 1998-December-02
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Microsoft Office 97
SEQ ID NO: 7
LENGTH: 923
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: unsure
LOCATION: (887)
FEATURE:
NAME/KEY: unsure
LOCATION: (895)
FEATURE:
NAME/KEY: unsure
LOCATION: (914)
US-09-452-239-7

```

```

Query Match 12.7%; Score 126; DB 4; Length 923;
Best Local Similarity 56.6%; Pred. No. 9,7e-16;
Matches 275; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

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QY 261 AGCCGCTTCATGCGGAGACCCGCGCTGCGAAGCTTGAGGCTGCTGACCTTGAGAGCAG 320
DB 138 ACCGCTCTCCACCGAGCCGAGCTGCTGCGGAGCTCGCGCCGACCGCCACCCAC 197
QY 321 CCGAGAGGGGATTCATGATACCTGCGAGAGCCAGCTCTTGCCCACTGAGCGG 380
DB 198 CCATGAGGGGAGCTGCTGCTGCGCGAGAGGAGTGAAGTGAAGTGAAGTGAAGTGAAG 257
QY 381 CTATTCAGAGCGCAAGAGGCGCTGAGCTTGAGCTTCAAGGCTTCTCGCCCTGAGCC 440
DB 258 ATTCTTGCGCGCAAGAGGCGCTGAGCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 317
QY 441 CTGAGCGCTGCGCTGCGCGCGAGCGGCGCTGAGCTTGAAGTGAAGTGAAGTGAAGTGAAG 500
DB 318 ACCGCTCTCCGCGCTGCGCGAGAGGAGCAAGTGTGCGCATGAGCTTACCGCGAGAGC 377
QY 501 CCGAGCTGAGAGCGGCGCTGAG---GCGAGCGCGAGCGGCGAGCGAGCGAGCTTCTC 557
DB 378 TACAGCAGATGAGGCTGCGCGGATGATGAGAGGCGCGCGAGCGAGCGAGCTTCTC 437
QY 558 CGGCTGAAGCGCGCGCTTGAAGACCTGAGAGCTGCTGAG---GCGCGCGAGCGCGCGC 614
DB 438 CGGCTGAGGCTGCGCGCTGCGCGCTGAGAGCGAGTGTGCGCGAGAGGAGGAGGAGGAGC 497
QY 615 ACCTTGAAGCGCGCTGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 674
DB 498 AAGTTCGAGCTTGAAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 557
QY 675 TGCGTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 734
DB 558 CTGCTGAAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 617
QY 735 AAGGTG 740
DB 618 TCCGTG 623

```

```

RESULT 14
US-07-708-866A-1
Sequence 1, Application US/0708866A
Patent No. 5322937
GENERAL INFORMATION:
APPLICANT: Arita Arisawa et al.
TITLE OF INVENTION: Genes Encoding A 3-Acylolation
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSES: Wenderoth, Lind & Ponack

```

```

STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Displaywrite
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/708,866A
FILING DATE: 19910531
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX: 202-371-8856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1810 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: No
ANTI-SENSE: No
ORIGINAL SOURCE:
ORGANISM: Streptomyces thermotolerans
STRAIN: ATCC 11416

```

```

FEATURE:
NAME/KEY: -35 signal
LOCATION: 120..125
IDENTIFICATION METHOD: S
FEATURE:
NAME/KEY: -10 signal
LOCATION: 143..148
IDENTIFICATION METHOD: S
FEATURE:
NAME/KEY: RBS
LOCATION: 194..198 AND 201..205
IDENTIFICATION METHOD: S
US-07-708-866A-1

```

```

Query Match 12.4%; Score 122.8; DB 1; Length 1810;
Best Local Similarity 58.5%; Pred. No. 4.3e-15;
Matches 233; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

```

```

QY 243 CTGAGCAATATCTTCTGAGCGCTTCATGCGGAGAGACCCGCGCTGCGAAGCTTGAAG 302
DB 1412 CTGAGCAATATGCGAGAGAGCTTCTGCGCGAGAGAGCGCGCTGCGAGCTGCGG 1471
QY 303 CTGCTGAGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 359
DB 1472 GAGTGAAGCGCGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1531
QY 360 CTCTTGCCCAAGCTGAGCGGCTTCATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 419
DB 1532 CTCTTGCGGCTGCTCATCGGCTTCAGCGGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 1591
QY 420 ACGGCTATTCGCGCGCTGAGCGCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 479
DB 1592 ACCGGGTACAGAGCTGATGATGAGCGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1651
QY 480 TCGAGAGTGAAGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 539
DB 1652 TCGAGATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 1711
QY 540 GAGCAGAGATGAGCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGC 599

```

Db 1712 GCCGACCCGATCGACTTCCGATCGGCGAGCCGCCGAGACCTCTGCGAGCTGCGTGA 1771  
 QY 600 GCGGCGAGGCGCCGACCTTGCAGCTGCGCCGCTGTGA 637  
 Db 1772 CACGAAGCGGACGCGATCTTGCAGCTGTGTGTGCTGA 1809

RESULT 15  
 US-07-708-866A-2  
 ; Sequence 2, Application US/07708866A  
 ; Patent No. 5322937  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Akira ARISAWA et al.  
 ; TITLE OF INVENTION: Gene Encoding A 3-Acylation  
 ; NUMBER OF SEQUENCES: 2  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Wenderoth, Lind & Ponack  
 ; STREET: 805 Fifteenth Street, N.W., #700  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: U.S.A.  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette, 5.25 inch, 500 Kb  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: MS-DOS  
 ; SOFTWARE: Displaywrite  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/07/708,866A  
 ; FILING DATE: 19910531  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Warren M. Cheek, Jr.  
 ; REGISTRATION NUMBER: 33,367  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-371-8850  
 ; TELEFAX: 202-371-8856  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1810 base pairs  
 ; TYPE: NUCLEIC ACID  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: unknown  
 ; US-07-708-866A-2

Query Match 12.4%; Score 122.8; DB 1; Length 1810;  
 Best Local Similarity 58.5%; Pred. No. 4.3e-15;  
 Matches 233; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 243 CTGTGGAGATATCTTGTGAGCCGCTCCATGCGGAGGACCCGCGCTGCGAGCTGAGG 302  
 Db 1412 CTGTGGAGATATCGCCAGGAGGCTCTCGCTGCGGACGACCGCTGTGCGCGAGCTGCGG 1471  
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 Job time : 96 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Sequence: 1 GCGGCGCCGCGAGTCGCGAGG.....CAAAAAAAAAAAAAAAAAAAAAA 989

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Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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2	989	100.0	989	6	AX697237
3	989	100.0	989	6	AX358476
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5	989	99.7	1041	9	BC047774
6	989	99.3	985	6	BD222712
7	989	94.9	988	9	AK074421
8	907.8	91.8	913	9	BC023663
9	789	73.8	789	6	AX338456
10	625	63.2	946	10	BC049670
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13	256.8	26.0	38679	9	AL390034
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DEFINITION	Sequence	21 from Patent WO0153466.				
ACCESSION	AX201342					
VERSION	AX201342.1	GI:15391164				
KEYWORDS						
SOURCE						
ORGANISM						
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	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
REFERENCE						
AUTHORS	1	Askenazi, A.J., Goddard, A., Godowski, P.J., Gurney, A.L.,				
	Hillan, K.J., Marsters, S.A., Pan, J., Pitti, R.M., Roy, W.A., Smith, V.,					
	Stone, D.M., Watanabe, C.K. and Wood, W.I.					

TITLE Compositions and methods for the treatment of tumor  
JOURNAL Patent: WO 0153486-A 21 26-JUL-2001;  
Genentech, Inc. (US)  
FEATURES Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 989; DB 6; Length 989;  
Best Local Similarity 100.0%; Pred. No. 3,7e-125;  
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS Sequence 305 from Patent W0078961.  
DEFINITION  
ACCESSION AX697237  
VERSION AX697237.1 GI:29498404  
KEYWORDS  
SOURCE  
ORGANISM  
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## REFERENCE

1 Ferrara, N., Stewart, T.A., Williams, P.M., Baker, K.P., Desnoyers, L.,  
Baton, D.L., Gao, W.Q., Pan, J., Botstein, D., Fong, S., Goddard, A.,  
Godowski, P.J., Gueney, A.L., Smith, N.F., Tuma, D., Wood, W.I.,  
Grimaldi, C.J., Hillan, K.J., Paoni, N.V., Roy, M.A. and Watanabe, C.K.  
Secreted and transmembrane polypeptides and nucleic acids encoding  
the same  
Patent: WO 0078961-A 305 28-DEC-2000;  
Genentech Inc. (US)

## JOURNAL

## TITLE

## AUTHORS

## FEATURES

## source

## ORIGIN

Query Match 100.0%; Score 989; DB 6; Length 989;  
Best Local Similarity 100.0%; Pred. No. 3,7e-125;  
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCCCGGAGTCCGAGACTGTCCAGAGACTCCAGCTCAAGTGAAGTCTGTACTGCG 60  
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QY	961	GCTGGGAC	CACAAAAAATTTTTTTTTTTT	989
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REFERENCE	AUTHORS	TITLE
1	Meyers, R.A. and Williamson, M.	25692, a novel human o-methyltransferase family member and uses

JOURNAL Patent: WO 0183719-A 1 08-NOV-2001; Millennium Pharmaceuticals, Inc. (US)

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VERSION	BC047774.1				
KEYWORDS	MGC.				
SOURCE	Homo sapiens (human)				
ORANISM	Homo sapiens				

REFERENCE  
AUTHORS

1 (bases 1 to 1041)

Strausberg, R. L., Fellnagold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shennan, C. M., Schaller, C. D., Eickholt, J. D., Zeeberg, B., Butler, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Datchenko, L., Marusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Shapiro, M., Soares, M. B., Batalov, M. F., Casavant, T. C., Scheetz, T. E., Brownstein, M. J., Udell, T. B., Tschuy, T. S., Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Canariini; Homnidae; Homo.

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,  
Abrahamson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Mortley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Rahy, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S.,  
Santchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalski, U., Smailus, D.E.,  
Scherer, A., Schein, J.R., Jones, S.J. and Marra, M.A. 2002  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL  
MEDLINE  
PUBMED  
22388257  
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2 (bases 1 to 1041)

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
DIRECT SUBMISSION  
Submitted (03-MAR-2003) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
Contact: MGC help desk  
Email: [gcgaps-remail.nih.gov](mailto:gcgaps-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [mc8pax11.stanford.edu](mailto:mc8pax11.stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
R. M.

REMARK  
COMMENT

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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Lal, P., Tang, Y.T., Gorgone, G.A., Corley, N.C., Guegler, K.J., Baughn, M.R., Akerbloom, I.E., Young, J.A., Yue, H., Patterson, C., Reddy, R., Hillman, J.L. and Bandman, O.  
 TITLE Human signal peptide-containing protein  
 JOURNAL Patent: JP 2002519030-A 58 02-JUL-2002;  
 INCYTE PHARMACEUTICALS INC  
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 OS Homo sapiens (human)  
 PN JP 2002519030-A/58  
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 PI MARIAN R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,  
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 ACCESSION AK074421  
 VERSION AK074421.1 GI:18677019  
 KEYWORDS oligo capping, fls (full insert sequence).  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Taishiro, H., Ota, T., Suzuki, Y., Ohashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.  
 TITLE NEDO human cDNA sequencing project  
 JOURNAL Direct SubMISSION  
 Submitted (14-FEB-2002) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan  
 (E-mail: flcdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

## COMMENT

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5' - & 3' - end one pass sequencing: Department of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology Agency).

## FEATURES

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## CDS

ORIGIN

Query Match 94.9%; Score 938.2; DB 9; Length 988;  
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VERSION BC023663.2 GI:40226187  
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ORGANISM Homo sapiens

REFERENCE  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenner, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schenker, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stjepeton, M., Soares, M.B., Bonaldo, M.F., Casavant, J.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Miliady, S.J., Bosak, S.A., McMan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Morley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulik, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Rahy, U., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shenchenko, Y., Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywicki, M.I., Skalek, U., Smalhe, D.E., Scherch, A., Schein, J.E., Jones, S.J. and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
2 (bases 1 to 913)  
Direct Submission  
Submitted (05-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK  
COMMENT NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
On Dec 19, 2003 this sequence version replaced gi:23959051.  
Contact: MGC help desk  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
Tissue Procurement: ATCC  
cDNA Library Preparation: Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)  
cDNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),

Gaithersburg, Maryland;  
Web site: <http://www.nisc.nih.gov/>  
Contact: [misc\\_mgc@nigr.nih.gov](mailto:misc_mgc@nigr.nih.gov)

Blakeley, R.W., Boultard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Latic, P., Legaspi, R., Madsen, Q.L., Mastello, C., Maskeri, B., Mastrian, S.D., McElroy, J.C., McDowell, J., Pearson, R., Stantford, S., Thomas, P.J., Touchman, J.W., Tsurgren, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H., and Green, E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: <http://image.llnl.gov>  
Series: IPAL, Plate: 39 Row: 3 Column: 6  
This clone was selected for full length sequencing because it passed the following selection criteria: Genomescan gene prediction, similarity but not identity to protein.

## FEATURES

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## CDS

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REFERENCE  
1 Meyers, R.A. and Williamson, M.  
25692, a novel human O-methyltransferase family member and uses  
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Patent: WO 0183719-A 3 08-NOV-2001;  
JOURNAL Millennium Pharmaceuticals, Inc. (US)  
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Dh      421 GAGCTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Qy      564 AAGCCCGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623
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Qy      804 CGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
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Qy      864 AAGATCTAG 872
Dh      781 AAGATCTAG 789

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RESULT 10
LOCUS   BC049670          946 bp      mRNA      linear      ROD 07-OCT-2003
DEFINITION Mus musculus RIKEN cDNA 1810030M08 gene, mRNA (cDNA clone MGC:58496
ACCESSION BC049670
VERSION   BC049670.1 GI:29612504
KEYWORDS MGC.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            1 (bases 1 to 946)
REFERENCE Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
AUTHORS   Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schley, G.D.,
            Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
            Hopkins, R.F., Jordan, H., Moore, T., Max, S.T., Wang, J., Hsieh, F.,

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Diatchenko L., Marusik K., Farmer A.F., Rubin, G.M., Hong, L.,
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 Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.N.,
 Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalhus, D.E.,
 Scherch, A., Schein, J.E., Jones, S.J., Skalska, U., Smalhus, D.E.,
 Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

NIH-MGC Project URL: <http://mgc.nci.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Michael Brownstein / Ted Udell

Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)

DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada

info@bgsbc.bc.ca  
 Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
 Susanna Chan, Readman Chiu, Chris Fell, Erin Garland, Ran Guin,
 Leticia Hsiao, Martin Krzywinski, Reta Kusche, Oliver Lee, Soo
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
 Nees, Pawan Pandoh, Anna-Lisa Prabhu, Parvaneh Saeedi, Jacqueline
 Schein, Duane Smalhus, Michael Smith, Loraine Spence, Jeff Stott,
 Michael Thorne, Miranda Tsai, Natasja van den Bosch, Jill Vardy,
 George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>  
 Series: ISAL Plate: 45 Row: B Column: 4.

Location/Qualifiers  
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Matches 745; Conservative 0; Mismatches 180; Indels 2; Gaps 1;

QY 63 CCGCCGCTCTCTGCGCGGCAATGACCCAGCCGGTGGCCGCTCTCCGTCGCCCGCG 122
DB 13 CCGCCGCTCTAACCCTGACACATGCTCAGCCCGCTCCCTCGCTATCTATCCACGCGCA 72
QY 123 CTGGCCCTGGGCTCAAGCCGCACTGGGGCGCGCTTGGCCACTGGGCTCTTCTGGGGAGG 182
DB 73 CTGGCCCTGGGCTCAAGCCGCGCTGGGGCGCGCTTGGCCACTGGGCTCTTCTGGGGAGG 132
QY 183 CCGTGGCCCCCAATGGCGAGGCGCGCGAGAGCAATGCTCTTCCCGCCGAGAGACGCGC 242
DB 133 CCGTGGCTCCATGGGGGTCCAGGCGCGAGAGCGCGCTGTCACCTGAGAGCAATCC 192
QY 243 CTGGGGAGATCTCTCTGAGCGGCTCCATGGCGAGAGCAAGCGCGCTGGAGAGCTAGG 302
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QY 363 TTGGCCAACTTGGCGCGGCTCATCAAGGCAAGAAAGGCTGGAGACTTGGGCACTTCAAG 422
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DB 373 GGCTACTCGGCTCTGAGCGGCTTGGCGCTTGGCGGCTGCGCGGAGAGCGGCGCGTGGTACCTGC 432
QY 483 GAGGTGAGAGCGGCAAGCCCGGAGGCTGGAGAGCGGCTTGGAGAGGCGAGAGCGGAG 542
DB 433 GAGGTGAGAGCGGCAAGCCCGGAGGCTGGAGAGCGGCGGAGGAGGAGGAGGAGGAG 492
QY 543 CACAAGATGACCTCGGCGTGAAGCGCGCTTGGAGAGCCGCGAGAGAGCTGCTGGCGGCG 602
DB 493 CAGAAGATGACCTTGGCGTGAAGCGCGCTTGGAGAGCCGCGAGAGAGCTGCTGGCGGCG 552
QY 603 GCGGAGCGCGGAGCACTTGGCGTGGCGGCTGGAGAGGAGAGCTGCTGGCGGCGGCG 662
DB 553 GCGGAGCGCGGAGCACTTGGCGATAGCGGCTGGAGAGGAGAGAGAGAGAGAGAGAGAG 612
QY 663 TACTACGAGCGGCTGCTGAGGCTGCTAGGCTCCCGAGAGGAGGCTGCTGCTAGAGTC 722
DB 613 TACTACGAGCGGCTGCTGAGGCTGCTAGGCTCCCGAGAGGAGGCTGCTGCTAGAGTC 672
QY 723 CTGTGGCGGAGAGGAGTGTGCAACCTCGAAGAGGAGAGCTGGCGGCGAGTGTGTGGA 782
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QY 783 AACCTTAAGAGAGAGAGTGTGCAAGGAGTGTGCAAGGAGTGTGTGTGTGTGTGTGTGT 842
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RESULT 11
AX407985/c      326 bp      DNA      linear      PAT 14-JUN-2002
LOCUS
DEFINITION
Sequence 632 from Patent WO0229103.
ACCESSION
AX407985
VERSION
AX407985.1 GI:21440690
KEYWORDS
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE
1
Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
Gene expression profiles in liver cancer
Patent: WO 0229103-A 632 11-Apr-2002;
GENE LOGIC INC (US)
FEATURES
Location/Qualifiers
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1..326
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Best Local Similarity 99.7%; Pred. No. 4.4e-33;
Matches 323; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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DB 266 GCCGCTCTGAGAGTCTGTGTGGCGGAGAGTGTGTGCAACCTTCCGAAAGGAGAGCTGGCG 207
QY 768 GCCGATGTGTGTGGAACCTTAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 827
DB 206 GCCGATGTGTGTGGAACCTTAACGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 147
QY 828 CTCCTGCCCTGGGCGAGTGAAGTCACTTGGGCTTCAAGATCTAGAGGCTGGCCCTAGTG 887
DB 146 CTCCTGCCCTGGGCGAGTGAAGTCACTTGGGCTTCAAGATCTAGAGGCTGGCCCTAGTG 87
QY 888 AGTGGCTGAGAGGAGGTTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 947
DB 86 AGTGGCTGAGAGGAGGTTGCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 27
QY 948 AAAATAAGTGGGCTGGAGACA 971
DB 26 AAAATAAGTGGGCTGGAGACA 3

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LOCUS
DEFINITION
Rattus norvegicus clone CH230-34D17, WORKING DRAFT SEQUENCE, 2
unordered pieces.
ACCESSION
AC120475
VERSION
AC120475.7 GI:25137871
KEYWORDS
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE
Rattus norvegicus
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE
1 (bases 1 to 237829)

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## AUTHORS

Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Barnham, F., Bawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Caesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., L., Davis, C., Davy-Carroll, L., De Anda, C., Decker, D., Delgado, O., Denson, S., Deramo, C., Ding, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gbureck, E., Geer, K., Gill, R., Grady, M., Guerra, M., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogue, M., Hollins, B., Howell, S., Hu, Y., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolyet, A., Karpachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kover, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Loulseged, H., Lozada, R., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Mallory, K., Mangum, B., Mapus, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Mlosov, I., Mroczka, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Mundasa, M., Murphy, K., Nair, L., Nakevicius, O., Okwum, G., Olarunpase, A., Pal, S., Paks, K., Paternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Pioppert, F., Polidexter, A., Popovic, D., Primus, E., Pu, L., Pu, L., Puazo, M., Quiriz, J., Rachin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S., J., Sanders, W., Savary, G., Scheier, S., Scott, G., Shattman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smas, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sores, J., Steimle, M., Strong, R., Sutton, A., Swalek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D., Waldron, D., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, K., White, F., Williams, G., Willson, R., Wleczky, R., Woodson, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G., and Gibbs, R.A.

## TITLE

Direct Submission

## JOURNAL

2 (bases 1 to 237829)

## REFERENCE

Worley, K.C.

## AUTHORS

Submitted (07-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## TITLE

3 (bases 1 to 237829)

## JOURNAL

Rat Genome Sequencing Consortium.

## REFERENCE

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## AUTHORS

On Nov 20, 2002 this sequence version replaced gi:23267656.

## TITLE

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas

## JOURNAL

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence

contigs within a contig-scaffold that consist entirely of whole

genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: CXLR

Center clone name: CH230-34D17

Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 218320 bases at least Q40

Consensus quality: 223359 bases at least Q30

Consensus quality: 225092 bases at least Q20

Bermited insert size: 222440; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

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Db	82066	GAGCCTGCGACTGTGACCTCTGGAGCAGCCGCGAGGGGAGATTCTATATATGACCTGGAGCA	821253						
QY	353	GGCCAGACTCTTGGAGCCCACTGGGCGGCGCTCATTCACAGCCCAAGAGGCGCTGGACCTGGG	412						
Db	82126	GGCCCAACTCTGTGTCACTGTGCGCGGCTCATTCAGAGCCCAAGAGGCGCTGGATCTGGG	821895						
QY	413	CACCTTCAGGAGCTA-CTCCGCGCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTG	471						
Db	82186	TACTTTCACGGGGCTACTCCGCGCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTGCCCTTG	822455						
QY	472	TGGTGACCTCGAGGTGAGCGCGAGCCCGCGAGCTGGGACGAGCCCTGTGGAGGACAG	531						
Db	82246	TGGTGACCTCGAGGTGAGCGCGAGCCCGCGAGCTGGGACGAGCCCTGTGGAGGACAG	823075						
QY	532	CCGAGGCGGAGCACAAGATCGACCTCCGCGTGAAGCCCGCTTGAAGACCTTGAGACGAC	591						
Db	82306	CAGAGGTGAGCAGAAAGATCGAATTGCGCTGCGAGCCCGCTTGAGACCTTGTGATGAGT	823655						
QY	592	TGCTGGGCGGCGGCGGAGCCCGGACCTTGCACGTGCGCGCTGTGTGATGCGGACAAGAG	651						
Db	82366	TGCTGGGCGGCGGCGGAGCCCGGACCTTGCACGTGCGCGCTGTGTGATGCGGACAAGAG	824255						
QY	652	ACTGCTCCGCTACTACGAGCG	673						
Db	82426	CTGCTCGCACTCCTTACGCGCG	82447						
RESULT 13									
AL390034/C									
LOCUS	38679 bp	DNA	linear	PRI 01-JAN-2002					
DEFINITION	Human DNA sequence from clone RP11-37563 on chromosome 10, complete								
ACCESSION	AL390034								
VERSION	AL390034.23	GI:18041549							
KEYWORDS	HTG.								
SOURCE	Homo sapiens (human)								
ORGANISM	Homo sapiens								
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								
AUTHORS	Wray, P.								
TITLE	Direct Submission								
JOURNAL	Submitted (01-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: hunguery@sanger.ac.uk								
COMMENT	On Jan 2, 2002 this sequence version replaced gi:18031099. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.								
	This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; SW, SwissSpot; Tr, TREMBL; Wp, WormPeP. Information on the WormPeP database can be found at								
	http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at								
	http://www.sanger.ac.uk/HGP/Chr10								

FEATURES	Location/Qualifiers
SOURCE	1. 38679 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /chromosome="10" /clone="RP11-375G3" /clone_1lb="RPCT-11.2" 2961. 29121 /note="Sequence from uni-directional dGTP big dye terminator reads only."
misc_feature	
ORIGIN	
Query Match	26.0%; Score 256.8; DB 9; Length 38679;
Best Local Similarity	97.4%; Pred. No. 4.1e-26; Index 0; Gaps 0;
Matches 261; Conservative	0; Mismatches 7; Indels 0; Gaps 0;
Db	7761 CCGCGCCCTCCCGAGGTCCTGTGGCGCGGGAAGGTCTCAACCTCCGAAAGCGGACGT 7702
Oy	704 CCTGCGCGGTCCTCAAGATCCTGTGGCGCGGGAAGGTCTCAACCTCCGAAAGCGGACGT 763
Oy	764 GCGCGCGGAGTGTGTGTGGAACCTTAAACGAACCATCCGCGGGGAGAGTCAAGGTCTACAT 823
Db	7701 GCGCGCGGAGTGTGTGGAACCTTAAACGAACCATCCGCGGGGAGTCAAGGTCTACAT 7642
Oy	824 CAGCCTCCTGCGCCCTGCGGCGATGAGACACCTTGGCCTTCAAGATCTAGGGCTGGCCCT 883
Db	7641 CAGCCTCCTGCGCCCTGCGGCGATGAGACACCTTGGCCTTCAAGATCTAGGGCTGGCCCT 7582
Oy	884 AGTGAAGTGGCTCGAGGAAGGCTTCTCTGGGAACCCAGGAATTGACCTGAGTTTAA 943
Db	7581 AGTGAAGTGGCTCGAGGAAGGCTTCTCTGGGAACCCAGGAATTGACCTGAGTTTAA 7522
Oy	944 TTGGAATTAAGTGGGCTGGGACACA 971
Db	7521 TTGGAATTAAGTGGGCTGGGACACA 7494
RESULT 14	
AC027393/C	169612 bp DNA linear HTG 24-AUG-2002
LOCUS	Homo sapiens chromosome 10 clone RP11-770D23 map 10, WORKING DRAFT
DEFINITION	SEQUENCE, 28 unordered pieces.
ACCESSION	AC027393.3 GI:8076860
VERSION	AC027393.3
KEYWORDS	HTG; HTGS; PHASE1; HTGS_DRAFT.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 169612) Britten, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Baetsen, V., Beda, F., Boguski, V., Boulton, A., Cantle, A., Chappel, Y., Colangelo, M., Collins, S., Campopiano, A., Cooke, P., DeRubeis, K., Dewar, K., Diaz, J. S., Dodgson, S., Donnelly, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gargyala, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hargis, B., Heath, A., Horton, L.,
AUTHORS	2 (bases 1 to 169612) Unpublished
JOURNAL	
REFERENCE	
AUTHORS	



Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lacroque, K., Lamazares, R., Landers, T., Lehoczy, U., Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marcini, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R., Meldrum, J., Meneus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, U., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanil, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Testa, S., Theodore, J., Tirrell, A., Travers, M., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (30-MAR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 169612)

## TITLE

JOURNAL

## REFERENCE

AUTHORS

## TITLE

JOURNAL

## COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On May 25, 2000 this sequence version replaced g1:7652066.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WISR

Web site: <http://www-seq.wi.mit.edu>Contact: [sequence.submissions@genome.wi.mit.edu](mailto:sequence.submissions@genome.wi.mit.edu)

Project information

Center project name: L6572

Center clone name: 770.D.23

Summary Statistics

Sequencing vector: M13; M7815; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 155213 bases at least Q40

Consensus quality: 162022 bases at least Q30

Consensus quality: 164973 bases at least Q20

Insert size: 178000; agarose-fp

Insert size: 166912; sum-of-contigs

Quality coverage: 4.1 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 28 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

## FEATURES

source

FEATURES	source
1	1191: contig of 1191 bp in length
1192	1291: gap of 100 bp
1292	2404: contig of 1113 bp in length
2405	2504: gap of 100 bp
2505	3705: contig of 1201 bp in length
3706	3805: gap of 100 bp
3806	4734: contig of 929 bp in length
4735	4834: gap of 100 bp
4835	6570: contig of 1736 bp in length
6571	6670: gap of 100 bp
6671	8583: contig of 1913 bp in length
8584	8683: gap of 100 bp
8684	10250: contig of 1607 bp in length
10291	10390: gap of 100 bp
10391	11938: contig of 1548 bp in length
11939	12038: gap of 100 bp
12039	15839: contig of 3801 bp in length
15840	15939: gap of 100 bp
15940	19203: contig of 3264 bp in length
19204	19303: gap of 100 bp
19304	22581: contig of 3278 bp in length
22582	22681: gap of 100 bp
22682	24947: contig of 2266 bp in length
24948	25047: gap of 100 bp
25048	28157: contig of 3120 bp in length
28158	28267: gap of 100 bp
28268	32083: contig of 3816 bp in length
32084	32183: gap of 100 bp
32184	35533: contig of 3350 bp in length
35534	35633: gap of 100 bp
35634	41517: contig of 5884 bp in length
41518	41617: gap of 100 bp
41618	47143: contig of 5526 bp in length
47144	47243: gap of 100 bp
47244	51694: contig of 4451 bp in length
51695	51794: gap of 100 bp
51795	57570: contig of 5776 bp in length
57571	57670: gap of 100 bp
57671	63180: contig of 5520 bp in length
63181	63280: gap of 100 bp
63281	70708: contig of 7418 bp in length
70709	70808: gap of 100 bp
70809	78988: contig of 8180 bp in length
78989	79088: gap of 100 bp
79089	86527: contig of 7439 bp in length
86528	86627: gap of 100 bp
86628	99114: contig of 12487 bp in length
99115	99214: gap of 100 bp
99215	110221: contig of 11007 bp in length
110222	110321: gap of 100 bp
110322	123287: contig of 12366 bp in length
123288	123387: gap of 100 bp
123388	147877: contig of 2490 bp in length
147878	147977: gap of 100 bp
147978	169612: contig of 21635 bp in length.

Location/Qualifiers

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/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="10"

/map="10"

/clone="RP11-770D23"

/clone\_lib="RP11-11 Human Male BAC"

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/note="assembly\_fragment"

1292..2404

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2505..3705

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3806..4734

/note="assembly\_fragment"

clone\_end:77



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Query Match      26.0%; Score 256.8; DB 2; Length 169612;
Best Local Similarity 97.4%; Pred. No. 2.8e-26;
Matches 261; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY      704 CCTGCCCTCTCTCAAGTCTCTGTGGCGCGGAAAGGTGTGCAACCTCCGAAAGGGAGCT 763
DB      140411 CCCCCCCTCCCGCAGTCTGTGGCGGGAAGGTGTGCAACCTCCGAAAGGGAGCT 140352

QY      764 GCGGCGCAGTGTGTGCGAAACCTAAAGCAAGCATCCGCGGGAAGCTCAGAGGTCTACAT 823
DB      140351 GCGGCGCAGTGTGTGCGAAACCTAAAGCAAGCATCCGCGGGAAGCTCAGAGGTCTACAT 140292

QY      824 CAGCTCTCTGCCCTGTGGCGAGTGAAGTCACTTGTGCTTCAAGTCTAAGGCTGCCCCCT 883
DB      140291 CAGCTCTCTGCCCTGTGGCGAGTGAAGTCACTTGTGCTTCAAGTCTAAGGCTGCCCCCT 140232

QY      884 AGTAGTAGGAGCTCGAGGAGGAGTGTCTGGGAAACCCAGAAATTGACCTGAGTTTAAA 943
DB      140231 AGTAGTAGGAGCTCGAGGAGGAGTGTCTGGGAAACCCAGAAATTGACCTGAGTTTAAA 140172

QY      944 TTGGAATAAATGAAGTGGGCTGGGACACA 971
DB      140171 TTGGAATAAATGAAGTGGGCTGGGACACA 140144

RESULT 15
AL606832/c      AL606832      157428 bp      DNA      linear      ROD 14-MAR-2002
DEFINITION      Mouse DNA sequence from clone RP23-346G22 on chromosome 3, complete
sequence.
ACCESSION      AL606832
VERSION      AL606832.4
KEYWORDS      GI:19571952
SOURCE      HTG.
ORGANISM      Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      Garner P.
AUTHORS      1 (bases 1 to 157428)
TITLE      Direct Submission
JOURNAL      Submitted (14-MAR-2002) Wellcome Trust Sanger Institute, Hinxton,

```

```

COMMENT
Cambridgehire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Mar 21, 2002 this sequence version replaced gi:19031533.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw:
SWISSPROT; Tr: TrEMBL; Wp: WormPEP; Information on the WormPEP
database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-346G22 is
from the RPI-23 Mouse PAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
VECTOR: pBACE3.6
IMPORTANT: This sequence is not the entire insert of clone
RP23-346G22. It may be shorter because we sequenced overlapping
sections only once, except for a short overlap.
The true right end of clone RP23-346G22 is at 157428 in this
sequence. The true left end of clone RP23-49014 is at 39071 in this
sequence. The true right end of clone RP23-265019 is at 2000 in
this sequence.

FEATURES
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    /mol_type="genomic DNA"
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    /chromosome="3"
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    /clone_11b="RPI-23"
    /note="Sequence from overlapping clone RP23-49014
    (AL606747). Assembly confirmed by restriction digest."
    117168..117122
    /note="single clone region. Assembly confirmed by
    restriction digest data. Single read sequenced with dGTP
    big dye terminator chemistry."

ORIGIN
Query Match      22.7%; Score 224.6; DB 10; Length 157428;
Best Local Similarity 70.2%; Pred. No. 6.8e-22;
Matches 391; Conservative 0; Mismatches 124; Indels 42; Gaps 5;

QY      69 CCTCTGCCCGCGGCATGACCAAGCCGCTGCTCCGTGCGCGCGCTGCGCT 128
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QY      129 CTGGGCTCAGCGCACTGGGCGCGGCTTGGCGCACTGCGCTCTTCTCTGGGAGCGGTGC 188
DB      11867 CTGGGCTCAGCGCACTGGGCGCGGCTTGGCGCACTGCGCTCTTCTCTGGGAGCGGTGC 11809

QY      189 CCCCCATGGCGAGGCGCGG-----AGACAGTGTCTGTTCCCTCCCGAGACAGCC 240
DB      11808 CTTCCGTTGGGGGGGGGGGGGTATGAGCAGCAATGTGCTTGTCCACCTGAGGACATTC 11749

QY      241 GCGTGTGAGAGTATCTTGTAGCCGCTCATCGGGAGACACCGGCGTGCAGAGCTGA 300
DB      11748 CCGTGTGAGAGTATCTTGTAGAGTGTCTTATAGAGG-----GCTGAGAGAGCTGT 11698

QY      301 GCGTGTGAGAGCTTGTAGAGCGCGGAGGAGATTATATATGATGACTTGTGAGCAGGCGCCAGC 360
DB      11697 GATTGTGAGAGCTTGTGAGCGCGGAGGAGATTCCATGTATGTATGTGAAACAGGCGCCAGC 11638

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QY 361 TCTTGCCAACTTGGCGGCTCATCCAGGCCAAGAGCGCTGGACCTGGGCACCTTCA 420
Db 11637 TTTCGACCAACTGGCGCAGCTCATCAAGGCCAAGAGCTCTGGATCTGGGTACTTTCA 11578
QY 421 CGGCTACTCGGCTGGCCCTGGCCCTGGCGCTGGCCCGGAGCGGCGGCTGGTGTGACT 480
Db 11577 CGGCTACTCGATCTGGCCCTAGCTTGGCAATCCAGAGGCTATGACC----- 11528
QY 481 GCGAGGTGACCGCGCAGCCCGGAGCTGGGACGCGCCCTGTGGAGGCAAGCCGAGCGG 540
Db 11527 -----TGCAGAGGCCCGGAGGCTGGGACCACTTTGGAGGCAAGGCAAGTGG 11478
QY 541 AGCAAGATGACCTCGGCTGAAAGCCGCTTG----GAGACCTGGAGAGAGCTGCTG 596
Db 11477 AGCAAGATGACCTTTGGCTACAGCCCGCTGCAAGACAGACTTGGTTGAGCTCTG 11418
QY 597 GCGGCGGCGGAGGCGG 613
Db 11417 GTGAGGCGCAGGCCAG 11401

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Search completed: April 10, 2004, 15:25:42  
 Job time : 4168 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 09:41:29 ; Search time 472 Seconds

(without alignments)  
8901.415 Million cell updates/sec

Title: US-10-017-407a-305

Sequence: 1 gcgggccccgcagctccgcaga.....caaaaaaaaaaaaaaaaaa 989

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_29Jan04:\*  
1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	989	100.0	989	3	AAA37107 Human PRO
2	989	100.0	989	4	AAAF5419 DNA encoc
3	989	100.0	989	6	ABK40264 CNA encoc
4	989	100.0	989	8	ACD68458 Novel humn
5	989	100.0	989	8	ACH04560 Human CDX
6	989	100.0	989	8	ACD68104 Novel humn
7	989	100.0	989	9	ADC18174 Human PRO
8	989	100.0	989	9	ADD70820 Human CDX
9	989	100.0	989	9	ADD39897 Human CDX
10	989	100.0	989	9	ADD70343 Human CDX
11	989	100.0	989	9	ADD38464 Human CDX
12	989	100.0	989	9	ADD39420 Human CDX
13	989	100.0	989	9	ADD38943 Human CDX
14	989	100.0	989	9	ADD40374 Human CDX
15	989	100.0	989	9	ADE50595 Human CDX
16	989	100.0	989	9	ADE20207 Human CDX
17	989	100.0	989	9	ADE50118 Human CDX
18	989	100.0	989	9	ADE21676 Human CDX
19	985.8	99.7	6	ABA05419 Human O-T	
20	981.8	99.3	3	AAZ98166 Human PRO	
21	981.8	99.3	6	ABQ61039 Human PRO	
22	938.2	94.9	6	AAH33455 Human COI	
23	799.8	80.9	812	3	AACT6634 Human ORF

24	789	79.8	789	6	ABA05420
25	701.8	71.0	876	8	AAD56372
26	701	70.9	885	8	AAD56361
27	422	42.7	474	8	ACH35195
28	413	41.8	458	8	ACH35890
29	404.4	40.9	770	9	ADD34178
30	312	31.5	326	6	ABX94134
31	185.8	18.8	2381	2	AAQ44449
32	174.8	17.7	178	4	AAOC89765
33	161.8	16.4	953	6	ABX63429
34	159.2	16.1	1049	6	ABX63428
35	158.6	16.0	997	6	ABX63413
36	158.6	16.0	1338	7	ADA71076
37	157.2	15.9	1078	6	ABX63427
38	155.6	15.7	1018	6	ABX63424
39	154	15.6	891	6	ABX63407
40	153	15.5	77536	3	AAA14651
41	152.8	15.4	1112	8	ADA49019
42	152.4	15.4	1218	2	AAZ52315
43	152.4	15.4	1218	5	AAZ05742
44	151.4	15.3	82746	7	AAH61224
45	149.2	15.1	666	7	ABZ40101

## ALIGNMENTS

RESULT 1	AAA37107	standard; cDNA, 989 BP.
ID	AAA37107	
AC	AAA37107;	
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DT	08-AUG-2000	(first entry)
DE	Human PRO1558 (UNQ766) cDNA sequence SEQ ID NO:305.	
XX		
KW	Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;	
XX	transmembrane; secretion; immunoadhesion; pharmaceutical; screening; se.	
OS	Homo sapiens.	
XX		
FN	WO200012708-A2.	
XX		
PD	09-MAR-2000.	
XX		
PF	01-SEP-1999;	99MO-US020111.
XX		
PR	01-SEP-1998;	98US-0098716P.
PR	01-SEP-1998;	98US-0098749P.
PR	02-SEP-1998;	98US-0098750P.
PR	02-SEP-1998;	98US-0098803P.
PR	02-SEP-1998;	98US-0098821P.
PR	09-SEP-1998;	98US-0098843P.
PR	09-SEP-1998;	98US-0098956P.
PR	09-SEP-1998;	98US-0098986P.
PR	09-SEP-1998;	98US-0099602P.
PR	10-SEP-1998;	98US-0099741P.
PR	10-SEP-1998;	98US-0099754P.
PR	10-SEP-1998;	98US-0099763P.
PR	10-SEP-1998;	98US-0099792P.
PR	10-SEP-1998;	98US-0099808P.
PR	10-SEP-1998;	98US-0099812P.
PR	10-SEP-1998;	98US-0099815P.
PR	10-SEP-1998;	98US-0099816P.
PR	15-SEP-1998;	98US-0100385P.
PR	15-SEP-1998;	98US-0100388P.
PR	15-SEP-1998;	98US-0100390P.
PR	16-SEP-1998;	98US-0100584P.
PR	16-SEP-1998;	98US-0100627P.
PR	16-SEP-1998;	98US-0100661P.

ABA05420	Human O-m
Aad56372	Human sec
Aad56361	Human sec
ACH35195	Human end
ACH35890	Human end
ADD34178	Mouse mit
ABX94134	Gene #632
AAQ44449	3-acylati
AAOC89765	Human gas
ABX63429	DNA encod
ABX63428	DNA encod
ABX63413	DNA encod
ADA71076	Rice gene
ABX63427	DNA encod
ABX63424	DNA encod
ABX63407	Nucleotid
AAA14651	Wheat gen
ADA49019	Maize caf
AAZ52315	Maize caf
AAZ05742	Actinosyn
AAH61224	N. gonorr
ABZ40101	

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PR 16-SEP-1998; 98US-0100662P.
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PR 17-SEP-1998; 98US-0100683P.
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PR 20-OCT-1998; 98US-0105000P.
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PR 22-OCT-1998; 98US-0105169P.
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PR 29-OCT-1998; 98US-0106384P.
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PR 30-OCT-1998; 98US-0106464P.

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PR 18-NOV-1998; 98US-0108851P.
PR 18-NOV-1998; 98US-0108852P.
PR 18-NOV-1998; 98US-0108858P.
PR 18-NOV-1998; 98US-0108904P.
PR (GENENTECH INC.
PA Baker K, Goddard A, Gurney AL, Smith V, Watanabe CK, Wood WI;
PI WPI; 2000-237671/20.
DR F-PSDB; AAY99425.
DR New mammalian DNA sequences encoding transmembrane, receptor or secreted
PT polypeptides, useful for screening of potential peptide or small
PT molecule inhibitors of the relevant receptor/ligand interactions.
XX Claim 2; Fig 171; 773pp; English.
XX
XX AAA37022 to AAA37144 encode the new isolated human transmembrane,
CC receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The
CC transmembrane and receptor PRO proteins can be used for screening of
CC potential peptide or small molecule inhibitors of the relevant
CC receptor/ligand interactions. The polypeptides and nucleotide sequences
CC encoding them have various industrial applications, including uses as
CC pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR
CC primers and hybridisation probes used in the isolation of the PRO
CC polypeptides from the present invention
XX
XX Sequence 989 BP; 169 A; 335 C; 335 G; 150 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 989; DB 3; Length 989;
Best Local Similarity 100.0%; Pred. No. 3.6e-156;
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GCGGGCCCGCAGTCCGAGACTGTCCTCCAGAGAGCTCCAGCTGACTGACTGCTCC 60
DB 1 GCGGGCCCGCAGTCCGAGACTGTCCTCCAGAGAGCTCCAGCTGACTGACTGCTCC 60
QY 61 TCCCGCGGCTCTCTCCGCGCGCATGACCGCGGCTCCCGGCTCTCCGTCGCGCG 120
DB 61 TCCCGCGGCTCTCTCCGCGCGCATGACCGCGGCTCCCGGCTCTCCGTCGCGCG 120
QY 121 CCGTGGCCCTGGGCTCGAGCGGCACTGGGCGCGGCTTGGCACTGCTCTTCCCTGGGGA 180
DB 121 CCGTGGCCCTGGGCTCGAGCGGCACTGGGCGCGGCTTGGCACTGCTCTTCCCTGGGGA 180
QY 181 GCGGGTGGCCCCCATGAGCGAGCGCGGAGAGAGAGTGCCTGCTCCCGCGAGACAGCC 240
DB 181 GCGGGTGGCCCCCATGAGCGAGCGCGGAGAGAGAGTGCCTGCTCCCGCGAGACAGCC 240
QY 241 GCGTGTGGAGTATCTTCTTGAAGCCGCTCAAGCGGAGAGACCCCGGCGCTGGAAGCTTGA 300
DB 241 GCGTGTGGAGTATCTTCTTGAAGCCGCTCAAGCGGAGAGACCCCGGCGCTGGAAGCTTGA 300

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QY 301 GGCTGCTGACCCCTGGAGCAGCCGAGGAGTTCTATGATGACCTGCGAGCAGGCCAGC 360  
 Db 301 GGCTGCTGACCCCTGGAGCAGCCGAGGAGTTCTATGATGACCTGCGAGCAGGCCAGC 360  
 QY 361 TCTTGCCCAACCTGAGCGGCTCATCCAGGCAAGAGGCGCTGAGACCTGGGACCTTCA 420  
 Db 361 TCTTGCCCAACCTGAGCGGCTCATCCAGGCAAGAGGCGCTGAGACCTGGGACCTTCA 420  
 QY 421 CGGAGTACTCCGCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCT 480  
 Db 421 CGGAGTACTCCGCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCT 480  
 QY 481 GCGAGTGAAGCAGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 540  
 Db 481 GCGAGTGAAGCAGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 540  
 QY 541 AGCAACAAGATGACCTCCGCTGAGAGCCGCTTGAAGACCTGAGACCTGAGACCTGAGC 600  
 Db 541 AGCAACAAGATGACCTCCGCTGAGAGCCGCTTGAAGACCTGAGACCTGAGACCTGAGC 600  
 QY 601 CGGCGAGCGCGAGCCTTGAAGACCTGAGAGCGCGCTGAGAGCGCGCTGAGAGCGCG 660  
 Db 601 CGGCGAGCGCGAGCCTTGAAGACCTGAGAGCGCGCTGAGAGCGCGCTGAGAGCGCG 660  
 QY 661 CCTACTAGAGCGCTGCTGAGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 720  
 Db 661 CCTACTAGAGCGCTGCTGAGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 720  
 QY 721 TCTGCTGCGCGAGAGAGTGTGCAACCTCCGAAAGCGAGCGCGAGCGCGAGCGCGAG 780  
 Db 721 TCTGCTGCGCGAGAGAGTGTGCAACCTCCGAAAGCGAGCGCGAGCGCGAGCGCGAG 780  
 QY 781 GAAACCTAAAGCAAGCAGTCCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 840  
 Db 781 GAAACCTAAAGCAAGCAGTCCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAG 840  
 QY 841 GCGATGAGACTCACTTGGCTTCAAGATCTAGAGGCTGCGCTGAGTGAAGTGGCTGAG 900  
 Db 841 GCGATGAGACTCACTTGGCTTCAAGATCTAGAGGCTGCGCTGAGTGAAGTGGCTGAG 900  
 QY 901 GAGGCTTGGCTGAGAGCGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960  
 Db 901 GAGGCTTGGCTGAGAGCGCGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 960  
 QY 961 GCTGGAACACAAAAAAGAAAAA 989  
 Db 961 GCTGGAACACAAAAAAGAAAAA 989

RESULT 2  
 AAF54419  
 ID AAF54419 standard; DNA; 989 BP.

XX AAF54419;  
 AC  
 DT 02-APR-2001 (first entry)  
 DE DNA encoding protein of the invention #84.  
 KM Secreted; transmembrane; gene therapy; ss.  
 OS Unidentified.  
 XX  
 XX WO200078961-A1.  
 XX  
 XX 28-DEC-2000.  
 PD  
 XX 18-FEB-2000; 2000WO-US004342.  
 PF  
 XX 23-JUN-1999; 99US-0141037P.  
 PR 20-JUL-1999; 99US-0144758P.  
 PR 26-JUL-1999; 99US-0145698P.

PR 01-SEP-1999; 99WO-US020111.  
 PR 29-OCT-1999; 99US-0162506P.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 02-DEC-1999; 99WO-US028551.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 XX  
 PA (GENTECH) GENENTECH INC.  
 XX  
 PI Baker KP, Botstein D, Deenoyers L, Baton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tamas D, Watanabe CK,  
 PI Williams PM, Wood WT;  
 XX  
 DR WPI, 2001-071395/08.  
 XX  
 PT Secreted and transmembrane proteins and nucleic acids designated PRO,  
 PT useful as hybridization probes, in chromosome and gene mapping and gene  
 PT therapy.  
 PS  
 PS Claim 2; Fig 167; 787bp; English.  
 XX  
 CC The present invention relates to secreted and transmembrane proteins.  
 CC These proteins and the DNA encoding them may be used as hybridization  
 CC probes, in chromosome and gene mapping and in the generation of anti-  
 CC sense RNA and DNA. They may also be used to generate either  
 CC transgenic animals or knockout animals which are in turn useful for  
 CC development and screening of therapeutically useful reagents. The nucleic  
 CC acids may also be used in gene therapy  
 XX  
 SQ Sequence 989 BP; 169 A; 335 C; 335 G; 150 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 989; DB 4; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3,6e-156;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GCGGCGCGCGAGTCCGAGACCTGTCCGAGAGCTCCAGTCACTGACTGCTGCTGCC 60  
 Db 1 GCGGCGCGCGAGTCCGAGACCTGTCCGAGAGCTCCAGTCACTGACTGACTGCTGCC 60  
 QY 61 TCCGCGCGCGCTCCG 120  
 Db 61 TCCGCGCGCGCTCCG 120  
 QY 121 CGCTGCGCGCTGAGCG 180  
 Db 121 CGCTGCGCGCTGAGCG 180  
 QY 181 GCGGCTGCG 240  
 Db 181 GCGGCTGCG 240  
 QY 241 GCGTGGCAGATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCGTGGAGACCTGA 300  
 Db 241 GCGTGGCAGATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCGTGGAGACCTGA 300  
 QY 301 GCGTGGCAGATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCGTGGAGACCTGA 360  
 Db 301 GCGTGGCAGATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCGTGGAGACCTGA 360  
 QY 361 TCTTGCCCAACCTGAGCGGCTCATCCAGGCAAGAGGCGCTGAGACCTGGGACCTTCA 420  
 Db 361 TCTTGCCCAACCTGAGCGGCTCATCCAGGCAAGAGGCGCTGAGACCTGGGACCTTCA 420  
 QY 421 CGGAGTACTCCGCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCT 480  
 Db 421 CGGAGTACTCCGCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCTGAGCCT 480  
 QY 481 GCGAGTGAAGCAGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 540  
 Db 481 GCGAGTGAAGCAGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCGAGCGCG 540

QY	544	AGCACAAGATTCGACCTCCCGGCTGAAGCCCGCCTTGAGACCTCGACGAGCTGCTGCAG	6000
QY	544	AGCACAAGATTCGACCTCCCGGCTGAAGCCCGCCTTGAGACCTCGACGAGCTGCTGCAG <td>6000</td>	6000
Db	541	AGCACAAGATTCGACCTCCCGGCTGAAGCCCGCCTTGAGACCTCGACGAGCTGCTGCAG	6000
QY	601	CGGCGCAGGCGCCGACCTTCGACGTGCGCTGTGTGATTCGCGACAGGAGATCTGCTCCG	6600
QY	601	CGGCGCAGGCGCCGACCTTCGACGTGCGCTGTGTGATTCGCGACAGGAGATCTGCTCCG	6600
Db	601	CGGCGCAGGCGCCGACCTTCGACGTGCGCTGTGTGATTCGCGACAGGAGATCTGCTCCG	6600
QY	661	CCTACTACGAGCGCTCCTGTCGACGTGTCGACCCGAGAGATCCTCGCCGCTCCAGAG	7200
Db	661	CCTACTACGAGCGCTCCTGTCGACGTGTCGACCCGAGAGATCCTCGCCGCTCCAGAG	7200
QY	721	TCTGTGTGCGCGGAGAGGTGCTGTCGAACTTCGAAAGGGGACGTGCGCGCAGTGTGTGC	7800
Db	721	TCTGTGTGCGCGGAGAGGTGCTGTCGAACTTCGAAAGGGGACGTGCGCGCAGTGTGTGC	7800
QY	781	GAACACCTAAACGAGACGCATCCGCGCGGACGTGAGGGGTCTACATGAGCTCCTGCGCCCTG	8400
Db	781	GAACACCTAAACGAGACGCATCCGCGCGGACGTGAGGGGTCTACATGAGCTCCTGCGCCCTG	8400
QY	841	GCAGTGCAGCTACCTCTTGCGCTTCAGATCTAAGGCTGTGCCCCCTTACGTAGTGTGCGAG	9000
Db	841	GCAGTGCAGCTACCTCTTGCGCTTCAGATCTAAGGCTGTGCCCCCTTACGTAGTGTGCGAG	9000
QY	901	GAGGGTTCCTGTGGAGACCCGAGGAAATTGACCTTGAGTTTAAATTGCAAAATAAGTGGG	9600
Db	901	GAGGGTTCCTGTGGAGACCCGAGGAAATTGACCTTGAGTTTAAATTGCAAAATAAGTGGG	9600
QY	961	GCTGGGACACAAAAAATAAAAAAATAAAAAA 969	
Db	961	GCTGGGACACAAAAAATAAAAAAATAAAAAA 969	

PX	(GETH ) GENENTECH INC.
PI	Ashkenazi AJ, Goddard A, Godowehi PJ, Gurney AL, Hillan KJ,
PI	Martens SA, Pan J, Pillel RM, Roy MA, Smith V, Stone DM;
PI	Matanabe CK, Wood WJ;
XX	WPI; 2002-205567/26.
DR	P-PDB: AA86138.
PT	Thirty five nucleic acids encoding PRO polypeptides, useful for treating
PT	benign or malignant tumors, leukemias and lymphoid malignancies,
PT	inflammatory, angiogenic and immunologic disorders.
XX	Claim 50; Fig 21; 302pp; English.
CC	The present invention relates to the isolation of novel human PRO
CC	polypeptides and the polymucleotide sequences encoding them. The PRO
CC	polypeptides, agonists, antagonists or anti-PRO antibodies are useful for
CC	treating benign or malignant tumors (e.g. renal, kidney, bladder,
CC	breast, etc), leukemias and lymphoid malignancies, other disorders such
CC	as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,
CC	stromal and blastococic disorders, inflammatory, immune and angiogenic
CC	disorders. The polymucleotide sequences are also useful in gene therapy.
CC	AAK40254-ABK40288 encode for the human PRO polypeptides of the invention
XX	
SQ	Sequence 969 BP; 169 A; 335 C; 335 G; 150 T; 0 U; 0 Other;
Query Match	100.0%; Score 989; DB 6; Length 989;
Best Local Similarity	100.0%; Pred. No.3,6e-156;
Matches 989; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 GCGGGCCCGCAGTCCGAGACCTGTCCAGAGAGCTCCAGTCACGTGACTGTCACTGCC 60
Ds	1 GCGGGCCCGCAGATCCGAGACTGTGCCAGAGAGCTCCAGCTCACGTGACTGTCACTGCC 60
QY	61 TCCC GCCGCTCTCTGCCCCGCGGCAGTAGACCAGCGGCGTGCCCCGCTCTCCGTCGCCGCCG 120
Ds	61 TCCC GCCGCTCTCTCTGCCCCGCGGCAGTAGACCAGCGGCGTGCCCCGCTCTCCGTCGCCGCCG 120
QY	121 CGCTGGCCCTTGAGGCTCAGCCGCACTGGAGCGCGCGCTTGCGCACTGAGCTCTTCTCTGGAGA 180
Ds	121 CGCTGGCCCTTGAGGCTCAGCCGCACTGGAGCGCGCGCTTGCGCACTGAGCTCTTCTCTGGAGA 180
QY	181 GGCGGTGCCCCCATAGGAGAGAGCGCGGAGACAGTCCGCTCCCGCCCGAAGAGACGCC 240
Ds	181 GGCGGTGCCCCCATAGGAGAGAGCGCGGAGACAGTGTCTGCTTCCCCCGAAGAGACGCC 240
QY	241 GCGTGGCAGTAATTCTTGAGCGCGCTTCAAGCGGAGACACCGCGGCTGTCAAAGCTTGA 3000
Ds	241 GCGTGGCAGTAATTCTTGAGCGCGCTTCAAGCGGAGACACCGCGGCTGTCAAAGCTTGA 3000
QY	301 GGTGTGTACCTTGAGAGACCGCAGGGGAGTTCTTAATGATGACTCGGAGACAGCCACG 360
Ds	301 GGTGTGTACCTTGAGAGACCGCAGGGGAGTTCTTAATGATGACTCGGAGACAGCCACG 360
QY	361 TCTTGGCCAACTGGCGCGGCTCATCCAGGCAAGAGCGCTGGAACCTTGAGCACTTCA 420
Ds	361 TCTTGGCCAACTGGCGCGGCTCATCCAGGCAAGAGCGCTGGAACCTTGAGCACTTCA 420
QY	421 CGGGCTACTCCGCGCTTGGCGCTGAGCGCTGAGCGCGGAGACGAGCGGCTGAGTACT 480
Ds	421 CGGGCTACTCCGCGCTTGGCGCTGAGCGCTGAGCGCGGAGACGAGCGGCTGAGTACT 480
QY	481 GCGAGGTGACGCGCAGCGCTCCGAGCTGGAGCGAGCGCTGTGTGAGCGACGCGAGCGG 540
Ds	481 GCGAGGTGACGCGCAGCGCTCCGAGCTGGAGCGAGCGCTGTGTGAGCGACGCGAGCGG 540
QY	541 AGCACAAGATGACCTCCGCGCTGGAAGCCCGCTTGAGAGACCTGTGAGAGACGACTGTGCGG 600
Ds	541 AGCACAAGATGACCTCCGCGCTGGAAGCCCGCTTGAGAGACCTGTGAGAGACGACTGTGCGG 600
QY	601 CGGCGAGGCGCGACCTTTCAGCTGAGCGCTGTGTGATGCGAGACAGAGAACTGCTCCG 666

Db 601 CGGCGAGGCGCGGACCTTGACCTGCGCCGTGGATGCGACAGAGAACTGCTCCG 660  
Qy 661 CCTACTACGAGCGCTGCTGAGTGTGCGACCCCGAGGCACTCTGCGCTCTCAGAG 720  
Db 661 CTTACTACGAGCGCTGCTGAGTGTGCGACCCCGAGGCACTCTGCGCTCTCAGAG 720  
Qy 721 TCTGTGCGCGGAGAGTGTGCAACCTCCGAAAGGAGAGCTGCGCGCGAGTGTGCG 780  
Db 721 TCTGTGCGCGGAGAGTGTGCAACCTCCGAAAGGAGAGCTGCGCGCGAGTGTGCG 780  
Qy 781 GAACTTAACGAGACGATCCGCGGAGACGTCAAGGCTTCACTACAGCTCTCCCTCG 840  
Db 781 GAACTTAACGAGACGATCCGCGGAGACGTCAAGGCTTCACTACAGCTCTCCCTCG 840  
Qy 841 GCGATGACTACCTTGCGCTTCAAGATCTAGAGGCTGCGCCCTAGTGTGCGTCTGAG 900  
Db 841 GCGATGACTACCTTGCGCTTCAAGATCTAGAGGCTGCGCCCTAGTGTGCGTCTGAG 900  
Qy 901 GAGGCTTGCCTGGGAGACCCCGAGATTGACCTTGAGTTTAATTGAAATTAAGTGG 960  
Db 901 GAGGCTTGCCTGGGAGACCCCGAGATTGACCTTGAGTTTAATTGAAATTAAGTGG 960  
Qy 961 GCTGGACACAAAAAATAAAAAA 989  
Db 961 GCTGGACACAAAAAATAAAAAA 989  
RESULT 4  
ACD68458 standard; cDNA; 989 BP.  
XX ACD68458;  
AC ACD68458;  
DT 17-SEP-2003 (first entry)  
XX  
XX  
XX Novel human secreted and transmembrane protein PRO1558 cDNA.  
XX  
XX Human; secreted and transmembrane protein; PRO; angiogenesis;  
KW endothelial cell proliferation; wound healing; immune response;  
KW T-lymphocytes proliferation; neonatal heart hypertrophy; tumour;  
KW cardiac insufficiency disorder; calcium flux; inflammation;  
KW vascular endothelial growth factor-stimulated proliferation;  
KW mammalian kidney mesangial cell proliferation; Berger disease;  
KW nephropathy; Schanlein-Henoch purpura; celiac disease; Crohn's disease;  
KW dermatitis herpetiformis; diabetes; haemoglobin switch; insulinemia;  
KW pancreatic beta-cell precursor cell differentiation; thalassemia;  
KW obesity; auditory hair cell regeneration; hearing loss; bone disorder;  
KW cartilage disorder; sports injury; arthritis; gene; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003073130-A1.  
XX  
XX PD 17-APR-2003.  
XX  
XX PF 11-DEC-2001; 2001US-00015869.  
XX  
XX 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
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PR 01-SEP-1998; 98US-0098750P.  
PR 02-SEP-1998; 98US-0098803P.  
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PR 16-SEP-1998; 98US-0100627P.  
PR 16-SEP-1998; 98US-0100661P.  
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PR 22-SEP-1998; 98US-0101279P.  
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PR 23-SEP-1998; 98US-0101472P.  
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PR 29-SEP-1998; 98US-0102330P.  
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PR 30-SEP-1998; 98US-0102484P.  
PR 30-SEP-1998; 98US-0102487P.  
PR 30-SEP-1998; 98US-0102570P.  
PR 30-SEP-1998; 98US-0102571P.  
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 PI Gao W, Goddard A, Godowsky FU, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
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 DR P-PSDB; ABO33667.  
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 PA (GETH ) GENENTECH INC.  
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 PI Baker KP, Boltstein D, Desnoyers L, Eaton DI, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
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 DR WPI; 2003-492259/46.  
 DR P-PSDB; ABO44520.  
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 PT Novel secreted and transmembrane polypeptides and polynucleotides  
 PT encoding them useful for treating various cardiac insufficiency  
 PT disorders, bone and/or cartilage disorders such as sports injuries and  
 PT arthritis.

Query Match 100.0%; Score 989; DB 8; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3, 6e-156; Indels 0; Gaps 0;  
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 PR 09-JUL-2001; 2001WO-US021735.

XX (GETH ) GENENTECH INC.

XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Goddard RJ, Grimaldi JC, Gurney AL, Hillan KJ;  
 PI Pan J, Pooni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
 PI Williams FW, Wood WI;

XX WPI; 2003-585292/55.  
 DR P-PSDB; ABO33544.

XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.

XX Claim 2; Fig 171; 561pp; English.

CC The invention describes an isolated PRO (secreted and transmembrane)  
 CC polypeptide (I), having at least 80% sequence identity to a sequence

Query Match 100.0%; Score 989; DB 9; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3; 66-156;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCCGCGAGTCCGAGACCTGCTCCGAGAGCTCCAGCTCAGTGCCTGTCACTGCC 60  
 DB 1 GGGGGCCGCGAGTCCGAGACCTGCTCCGAGAGCTCCAGCTCAGTGCCTGTCACTGCC 60  
 QY 61 TCCGCGCCGCTCTTCCGCGCCGATGACCCAGCCGCTGCTCCGCTCCGCGCCG 120  
 DB 61 TCCGCGCCGCTCTTCCGCGCCGATGACCCAGCCGCTGCTCCGCTCCGCGCCG 120  
 QY 121 CGCTGCGCTGCGCTCAGCGGCACTGGGCGCGCTTGGCCACTGGCTCTTCTCGGAG 180  
 DB 121 CGCTGCGCTGCGCTCAGCGGCACTGGGCGCGCTTGGCCACTGGCTCTTCTCGGAG 180  
 QY 181 GCGGCTGCGCTGCGCTCAGCGGCACTGGGCGCGCTTGGCCACTGGCTCTTCTCGGAG 240  
 DB 181 GCGGCTGCGCTGCGCTCAGCGGCACTGGGCGCGCTTGGCCACTGGCTCTTCTCGGAG 240

QY 241 GCTGTGCGAGTATCTTGTGAGCGCGCTCCATGCGGAGACCCGCGCTGCGAACTGA 300  
 DB 241 GCTGTGCGAGTATCTTGTGAGCGCGCTCCATGCGGAGACCCGCGCTGCGAACTGA 300  
 QY 301 GGTCTGTGACCTTGTGAGCAGCGCGGAGATTCTATATATGACTTGGAGAGAGCCAGC 360  
 DB 301 GGTCTGTGACCTTGTGAGCAGCGCGGAGATTCTATATATGACTTGGAGAGAGCCAGC 360  
 QY 361 TCTTGAGCAACTGTGCGCGCTCATTCAGGCAAGAGGCGCTGAGACCTTGAGCACTTCA 420  
 DB 361 TCTTGAGCAACTGTGCGCGGCTCATTCAGGCAAGAGGCGCTGAGACCTTGAGCACTTCA 420  
 QY 421 CGGCTACTCCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 480  
 DB 421 CGGCTACTCCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCTGCGCT 480  
 QY 481 GCGAGGTGAGCAGCGAGCGCGCGCGAGCTGAGAGCGCGCTGAGAGCGAGCGAGCGG 540  
 DB 481 GCGAGGTGAGCAGCGAGCGCGCGCGAGCTGAGAGCGCGCTGAGAGCGAGCGAGCGG 540  
 QY 541 AGCACAAGATGACCTTCCGCTGAAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGCGG 600  
 DB 541 AGCACAAGATGACCTTCCGCTGAAAGCCCGCTTGGAGACCTTGGACGAGCTGCTGCGG 600  
 QY 601 CGGCGAGCGCGCGCGCGCTTCCGCGCGCTGCGCGCTGCGCGCGCGCGCGCGCGCGG 660  
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 QY 721 TCTGTGCGCGCGGAGGCTGCGAGCTTCCGAGAGGCGAGCTGCGCGCGCGCGCGG 780  
 DB 721 TCTGTGCGCGCGGAGGCTGCGAGCTTCCGAGAGGCGAGCTGCGCGCGCGCGCGG 780  
 QY 781 GAAACCTAAGCAGAGCTCCGCGGAGCGTCAAGGCTTACATCAGCTCTGCGCGCTG 840  
 DB 781 GAAACCTAAGCAGAGCTCCGCGGAGCGTCAAGGCTTACATCAGCTCTGCGCGCTG 840  
 QY 841 GCGATGAGCTCACTTGGCTTCAAGATCTAGAGGCTGCGCGCTTCTGAGTGGCTCGAG 900  
 DB 841 GCGATGAGCTCACTTGGCTTCAAGATCTAGAGGCTGCGCGCTTCTGAGTGGCTCGAG 900  
 QY 901 GAGGTTGCTGAGAGCCGAGAGTGAACCTGAGTTTAAATCGAAATTAAGTGG 960  
 DB 901 GAGGTTGCTGAGAGCCGAGAGTGAACCTGAGTTTAAATCGAAATTAAGTGG 960  
 QY 961 GCTGGAGCAAAAATAAAAAAAAAAAAAA 989  
 DB 961 GCTGGAGCAAAAATAAAAAAAAAAAAAA 989

RESULT 7  
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 ID ADCL8174 standard; cDNA; 989 BP.

XX AC ADCL8174;  
 XX 18-DEC-2003 (first entry)  
 DE Human PRO polynucleotide #86.  
 XX Human; PRO; gene; ss; protein electrophoresis; chromosome mapping;  
 KW gene mapping; genetic disorder.  
 XX Homo sapiens.  
 XX US2003064925-A1.  
 XX 03-APR-2003.  
 XX 10-DEC-2001; 2001US-00013907.

XX  
PR 01-SEP-1998; 98US-0098716P.  
PR 01-SEP-1998; 98US-0098723P.  
PR 01-SEP-1998; 98US-0098749P.  
PR 01-SEP-1998; 98US-0098750P.  
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PR 29-OCT-1998; 98US-0108500P.  
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PR 03-NOV-1998; 98US-0106856P.  
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PR 03-NOV-1998; 98US-0106932P.  
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PR 10-NOV-1998; 98US-0107783P.  
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PR 30-DEC-1998; 98US-0114223P.  
PR 05-JAN-1999; 99US-0129674P.  
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PR 23-JUN-1999; 99US-0141037P.  
PR 26-JUL-1999; 99US-0144758P.  
PR 01-SEP-1999; 99US-0145698P.  
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PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99US-0162506P.  
PR 02-DEC-1999; 99US-0162506P.  
PR 16-DEC-1999; 99US-0162506P.  
PR 05-JAN-2000; 2000US-013705.  
PR 06-JAN-2000; 2000US-013705.  
PR 11-FEB-2000; 2000US-013705.  
PR 18-FEB-2000; 2000US-013705.  
PR 24-FEB-2000; 2000US-013705.  
PR 02-MAR-2000; 2000US-013705.  
PR 15-MAR-2000; 2000US-013705.  
PR 17-MAY-2000; 2000US-013705.  
PR 22-MAY-2000; 2000US-013705.

PR 30-MAY-2000; 2000MO-US014941.  
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 PR 24-AUG-2000; 2000MO-US023328.  
 PR 08-NOV-2000; 2000MO-US030952.  
 PR 10-NOV-2000; 2000MO-US030873.  
 PR 01-DEC-2000; 2000MO-US032678.  
 PR 28-FEB-2001; 2001MO-US006520.  
 PR 01-MAR-2001; 2001MO-US006666.  
 PR 01-JUN-2001; 2001MO-US017800.  
 PR 20-JUN-2001; 2001MO-US019692.  
 PR 29-JUN-2001; 2001MO-US021066.  
 PR 09-JUL-2001; 2001MO-US021735.  
 PR 04-SEP-2001; 2001US-00946374.  
 XX  
 XX (GENTH ) GENENTECH INC.  
 XX Baker KP, Botstein D, Deenoyers J, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams FM, Wood WI;  
 XX  
 XX WPI: 2003-555602/52.  
 DR P-PSDB; AOC18175.  
 XX  
 XX Novel isolated PRO polypeptides e.g. PRO1491 and PRO1571, useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide, and as therapeutic agents e.g. vaccines.  
 XX  
 XX Claim 2; SEQ ID NO 305; 555bp; English.  
 XX  
 CC The invention relates to human PRO polypeptides and the polynucleotides  
 CC encoding them. The sequences are useful in the preparation of a  
 CC medicament for treating a condition responsive to a PRO polypeptide. The  
 CC polypeptides are useful in a number of functional biological assays, as  
 CC molecular weight markers for protein electrophoresis and as therapeutic

Query Match 100.0%; Score 989; DB 9; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3.6e-156;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGGCCCGGAGTCCGAGCTGCTCCAGAGAGTCCAGCTCAGTACCTGTACTGCC 60  
 DB 1 GGGGGCCCGGAGTCCGAGCTGCTCCAGAGAGTCCAGCTCAGTACCTGTACTGCC 60  
 QY 61 TCCGCCGCTCTCTGCGCCGCGCATGACCCAGCCGCTGCTCCGTCGCGCCG 120  
 DB 61 TCCGCCGCTCTCTGCGCCGCGCATGACCCAGCCGCTGCTCCGTCGCGCCG 120  
 QY 121 CGCTGGCCCTGGGCTCAGCCGCACTGGGCGCGCTTCCGCACTGGGCTCTTCTG 180  
 DB 121 CGCTGGCCCTGGGCTCAGCCGCACTGGGCGCGCTTCCGCACTGGGCTCTTCTG 180  
 QY 181 GCGCGTGGCCCGCCATGAGCGAGCGCGAGAGAGTGCCTGCTTCCCGGAGAGACC 240  
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 DB 721 TCTGTGGCGCGGAGAGGTGTCTCAACCTCCGAAAGGAGAGCTGTGCGCGCGAGGTGTGTG 780  
 QY 781 GAACTCTAAGAGAGCACTCCGCGGAGAGCTGAGGCTTACATCAAGCTCTGCGCGCTGTG 840  
 DB 781 GAACTCTAAGAGAGCACTCCGCGGAGAGCTGAGGCTTACATCAAGCTCTGCGCGCTGTG 840  
 QY 841 GCGATGACTCACTTGGCTTCAAGATCTAGGCTGCGCCCTAGTGAAGTGGCTGAGG 900  
 DB 841 GCGATGACTCACTTGGCTTCAAGATCTAGGCTGCGCCCTAGTGAAGTGGCTGAGG 900  
 QY 901 GAGGCTGCTGCTGGAGAACCCAGAGATTGACCTTGATTTTAATTCGAAATTAAGTGG 960  
 DB 901 GAGGCTGCTGCTGGAGAACCCAGAGATTGACCTTGATTTTAATTCGAAATTAAGTGG 960  
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 DB 961 GCTGGAGACAAAAAAGAAAAAAGAAAAA 989  
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 XX ADD70820;  
 AC  
 XX 15-JUN-2004 (first entry)  
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 DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
 XX  
 KW Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schoulein-Henoch purpura; coeliac disease;  
 KW dermatitis; herpeticiformis; Cronh's disease; thalassemia.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003095625-A1.  
 XX  
 PD 29-MAY-2003.  
 XX  
 XX 12-DEC-2001; 2001US-00015386.  
 PF  
 XX 01-SEP-1998; 98US-0098716P.  
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 PR 01-SEP-1998; 98US-0098750P.  
 PR 02-SEP-1998; 98US-0098803P.  
 PR 02-SEP-1998; 98US-0098821P.  
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PR 03-NOV-1998; 98US-0106932P.  
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 (SETH ) GENENTECH INC.  
 PA Baker KP, Bolstein D, Desnoyers J, Eaton DI, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
 XX WPI; 2003-708344/67.  
 DR P-PSDB; ADD70344.  
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 PT Novel isolated PRO polypeptide useful for tissue typing, modulating  
 PT biological activity of cell, as molecular weight markers in protein  
 PT electrophoresis, for treating arthritis, tumor.  
 PS Claim 2; SEQ ID NO 305; 549pp; English.  
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 CC The invention relates to an isolated PRO polypeptide (secreted or  
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 KW immune response; cardiac insufficiency disorder; calcium flux;  
 KW umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KW arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KW Berger disease; nephropathy; Schönlein-Henoch purpura; celliac disease;  
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PR 02-MAR-2000; 2000US-0500584P.  
PR 15-MAR-2000; 2000US-0500684P.  
PR 17-MAY-2000; 2000US-0501705P.  
PR 22-MAY-2000; 2000US-0501404P.  
PR 30-MAY-2000; 2000US-0501494P.  
PR 02-JUN-2000; 2000US-0501526P.  
PR 23-AUG-2000; 2000US-0502352P.  
PR 24-AUG-2000; 2000US-0502328P.  
PR 08-NOV-2000; 2000US-0503095P.  
PR 10-NOV-2000; 2000US-0503087P.  
PR 01-DEC-2000; 2000US-0503267P.  
PR 28-FEB-2001; 2001US-05006520P.  
PR 01-MAR-2001; 2001US-0500666P.  
PR 01-JUN-2001; 2001US-0501780P.  
PR 20-JUN-2001; 2001US-0501692P.  
PR 29-JUN-2001; 2001US-0502106P.  
PR 04-SEP-2001; 2001US-0094637P.

XX (GETH ) GENENTECH INC.  
 PA Baker KP, Botstein D, Desnoyers L, Eaton DU, Ferrara N, Fong S,  
 XX Gao W, Goddard A, Goddard PJ, Grimaldi JC, Guirney AL, Hillan KJ,  
 PI Pan J, Pooni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams FM, Wood WI;  
 XX WPI; 2003-787000/74.  
 DR P-PSDB; ADD38465.  
 XX  
 PT Novel isolated PRO polypeptide, useful for treating cancerous tumors,  
 PT cardiac insufficiency disorders, wound healing, diabetes mellitus,  
 PT thalassemias.  
 PS Claim 2; SEQ ID NO 305; 556bp; English.  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 transmembrane protein) having at least 80% amino acid sequence identity

Query Match 100.0%; Score 989; DB 9; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3; ee-156;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGGGCCCGGAGTCCGAGACTGCTCCAGAGCTCCAGTCACTGTCAGTGC 60  
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 DB 61 TCCCGCCGCTTCCTGCGCCGCGCATGACCCAGCTGCGGCTCTCCGTCGCGCG 120  
 QY 121 CGCTGCGCCCTGCGCTCAGCGCAGTGGGCGCGGCTTGGCCACTGCGCTCTTCTGCGGA 180  
 DB 121 CGCTGCGCCCTGCGCTCAGCGCAGTGGGCGCGGCTTGGCCACTGCGCTCTTCTGCGGA 180  
 QY 181 GCGCGTGGCCCCCATGGAGCGCGCGAGAGCATGCTGCTTCCCGCGAGACAGCC 240  
 DB 181 GCGCGTGGCCCCCATGGAGCGCGCGAGAGCATGCTGCTTCCCGCGAGACAGCC 240  
 QY 241 GCGTGGGAGTATTTCTGAGCGGCTTCCAGCGGAGACACCGGCGCTCGGAAGCTTGA 300  
 DB 241 GCGTGGGAGTATTTCTGAGCGGCTTCCAGCGGAGACACCGGCGCTCGGAAGCTTGA 300  
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 QY 421 CGGGTATCTCGGCGCTTGGCGCTGCGCTGCGCGAGAGCGGCGCTGCTGACT 480  
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 QY 541 AGCAAGATGAGCTCGGCTGAGAGCGCGCTTGGAGAGCTTGAAGAGAGTGTGAGCGG 600  
 DB 541 AGCAAGATGAGCTCGGCTGAGAGCGCGCTTGGAGAGCTTGAAGAGAGTGTGAGCGG 600  
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 DB 961 GCTGGGACACAAAAA 989

## RESULT 12

ADD39420  
 ID ADD39420 standard; cDNA; 989 BP.

XX ADD39420;  
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DT 15-JAN-2004 (first entry)  
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DE Human cDNA encoding secreted/transmembrane protein PRO1558.  
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XX Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;  
 KM immune response; cardiac insufficiency disorder; calcium flux;  
 KM umbilical vein endothelial cell; bone disorder; cartilage disorder;  
 KM arthritis; wound healing; diabetes; skeletal muscle cells; obesity;  
 KM Berger disease; nephropathy; Schonlein-Henoch purpura; coeliac disease;  
 KM dermatitis; herpeticiformis; Crohn's disease; thalassemia.

OS Homo sapiens.  
 XX

PN US2003096954-A1.  
 XX

PD 22-MAY-2003.  
 XX

PF 07-DEC-2001; 2001US-00011671.  
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PR 01-SEP-1998; 98US-0098716F.  
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 PR 09-SEP-1998; 98US-0099602P.  
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PR 22-DEC-1998; 98US-0113296P.  
PR 30-DEC-1998; 98US-0114233P.  
PR 05-JAN-1999; 99US-05000106.  
PR 16-APR-1999; 99US-0129674P.  
PR 23-JUN-1999; 99US-0141037P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0146588P.  
PR 01-SEP-1999; 99US-05020111.  
PR 15-SEP-1999; 99US-05021194.  
PR 29-OCT-1999; 99US-0162506P.  
PR 30-NOV-1999; 99US-05028313.  
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PR 11-FEB-2000; 2000US-0500376.  
PR 18-FEB-2000; 2000US-0500365.  
PR 24-FEB-2000; 2000US-05004342.  
PR 02-MAR-2000; 2000US-05005884.  
PR 15-MAR-2000; 2000US-05006884.  
PR 17-MAR-2000; 2000US-05013705.  
PR 22-MAY-2000; 2000US-05014042.  
PR 30-MAY-2000; 2000US-05014941.  
PR 02-JUN-2000; 2000US-05015264.  
PR 23-AUG-2000; 2000US-05023522.  
PR 24-AUG-2000; 2000US-05023328.  
PR 08-NOV-2000; 2000US-05030952.  
PR 10-NOV-2000; 2000US-05030873.  
PR 01-DEC-2000; 2000US-05032678.  
PR 28-FEB-2001; 2001US-05006520.  
PR 01-MAR-2001; 2001US-05006666.  
PR 01-JUN-2001; 2001US-05017800.  
PR 20-JUN-2001; 2001US-05019692.  
PR 29-JUN-2001; 2001US-05021065.  
PR 09-JUL-2001; 2001US-05021735.  
PR 04-SEP-2001; 2001US-00946374.  
  
(GETH ) GENENTECH INC.  
XX Baker KP, Botstein D, Desnovers L, Eaton DL, Ferrara N, Fong S;  
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ;  
XX Pan T, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK;  
XX Williams PM, Wood WI;  
XX WPI; 2003-786999/74.  
XX P-PSDB; ADD39421.  
XX Novel isolated PRO polypeptide useful for tissue typing, modulating  
XX biological activity of cell, as molecular weight markers in protein  
XX electrophoresis, for treating arthritis, tumor.

PS Claim 2; SEQ ID NO 305; 550bp; English.

CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 989; DB 9; Length 989;

Best Local Similarity 100.0%; Pred. No. 3, 6e-156;

Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCGGCGCCCGGAGTCCGAGACCTGTCGAGAGCTCCAGCTCAGCTGACCTGCTACTGCC 60  
 DB 1 GCGGCGCCCGGAGTCCGAGACCTGTCGAGAGCTCCAGCTCAGCTGACCTGCTACTGCC 60  
 QY 61 TCCGCGCGGCTCTGCGCGCGCGCATGACCCAGCGCGGTCGCGCGGCTCTGCGCGCGCG 120  
 DB 61 TCCGCGCGGCTCTGCGCGCGCGCATGACCCAGCGCGGTCGCGCGGCTCTGCGCGCGCG 120  
 QY 121 CGCTGCGCGCTGAGCTCAGCCGCACTGCGCGCGCGCTTCGCCACTGCGCTCTTCTGCGGGA 180  
 DB 121 CGCTGCGCGCTGAGCTCAGCCGCACTGCGCGCGCGCTTCGCCACTGCGCTCTTCTGCGGGA 180  
 QY 181 GCGCGTGCCTCCCATGCGGAGCGCGGCGAGAGCACTGCTGCTTCCCGCGGAGAGACGCC 240  
 DB 181 GCGCGTGCCTCCCATGCGGAGCGCGGCGAGAGCACTGCTGCTTCCCGCGGAGAGACGCC 240  
 QY 241 GCGTGTGACAGTATCTTCTGAGCGGCTCCATGCGGAGACCCGCGCGCTGCGAGAGCTGA 300  
 DB 241 GCGTGTGACAGTATCTTCTGAGCGGCTCCATGCGGAGACCCGCGCGCTGCGAGAGCTGA 300  
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 DB 301 GCGCTGTGACCTCTGAGAGACCGCGAGGGGAGTTCTATGATGACCTGCGAGAGCGCTAGC 360  
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 DB 361 TCTTGAGCAACCTGAGCGGCTCATCCAGAGCGCAAGAGCGCTGAGCTGAGCGCACTTCA 420  
 QY 421 CGGCGTACTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCGAGCGCGCGCTGCTGACT 480  
 DB 421 CGGCGTACTCGCGCTGCGCTGCGCTGCGCTGCGCTGCGCGAGCGCGCGCTGCTGACT 480  
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 DB 601 CGGCGTGTGAGCGCGAGCGCGCGAGCGCGAGCGCGCGCTGAGAGCGCGCGAGCGCGCG 660  
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 QY 721 TCTGTGTGCGCGGAGAGCTGCTGCACTCCGAAAGGAGAGCTGCGCGAGAGCTGCTGCTG 780  
 DB 721 TCTGTGTGCGCGGAGAGCTGCTGCACTCCGAAAGGAGAGCTGCGCGAGAGCTGCTGCTG 780  
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 DB 841 GCGATGAGTCACTTGGCTTCAAGATCTAGGCTGCGCGCTGAGTGAAGTGGCTGAGG 900  
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 QY 961 GCTGGAGACACAAAAA 989

DB

961 GCTGGAGACACAAAAA 989

RESULT 13

ADD38943

ID ADD38943 standard; cDNA; 989 BP.

XX

ADD38943;

XX

15-JAN-2004 (first entry)

DE

Human cDNA encoding secreted/transmembrane protein PRO1558.

XX

Human; ss; gene; secreted protein; transmembrane protein; PRO; tumour;

KM

Immune response; cardiac insufficiency disorder; calcium flux;

KM

umbilical vein endothelial cell; bone disorder; cartilage disorder;

KM

arthritis; wound healing; diabetes; skeletal muscle cells; obesity;

KM

Berger disease; nephropathy; Schönlein-Henoch purpura; coeliac disease;

XX

dermatitis; herpeticiformis; Crohn's disease; thalassemia.

OS

Homo sapiens.

XX

US2003092061-A1.

XX

15-MAY-2003.

PD

06-DEC-2001; 2001US-00007194.

XX

01-SEP-1998; 98US-0098716P.

XX

01-SEP-1998; 98US-0098723P.

PR

01-SEP-1998; 98US-0098750P.

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02-SEP-1998; 98US-0098821P.

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02-SEP-1998; 98US-0098843P.

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XX (GENTH) GENENTECH INC.  
XX Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
XX Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AU, Hillan KJ, CK,  
XX Pan Y, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
XX Williams PW, Wood WI;  
XX  
XX MPI: 2003-765477/72.  
XX P-PSDB; ADD38944.  
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XX New isolated PRO polypeptide such as PRO1560, PRO444, PRO1018, PRO1773,  
XX PRO1244, PRO1246, useful for treating cancerous tumors, cardiac  
XX insufficiency disorders, wound healing, Crohn's disease, celiac disease.  
XX  
XX Claim 2; SEQ ID NO 305; 555bp; English.  
XX  
XX The invention relates to an isolated PRO polypeptide (secreted or  
XX  
CC  
  
Query Match 100.0%; Score 989; DB 9; Length 989;  
Best Local Similarity 100.0%; Pred. No. 3.6e-156;  
Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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 PR 05-JAN-1999; 99WO-US000106.  
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 PI Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S;  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillen KJ,  
 PI Pan J, Paoni NF, Roy MA, Smith V, Stewart TA, Tumas D, Watanabe CK,  
 PI Williams PM, Wood WI;  
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 DR WPI: 2003-755104/71.  
 DR P-PSDB; ADP40375.  
 XX  
 PT New isolated PRO polypeptides such as PRO1560, PRO444, PRO1018, PRO1773,  
 PT PRO1244, PRO1246, are useful for treating cancerous tumors and cardiac  
 PT insufficiency disorders.  
 XX  
 PS Claim 2; SEQ ID NO 305; 550bp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or  
 CC Query Match 100.0%; Score 989; DB 9; Length 989;  
 CC Best Local Similarity 100.0%; Pred. No. 3,6e-156;  
 CC Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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XX 29-JAN-2004 (first entry)
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XX umbilical vein endothelial cell; bone disorder; cartilage disorder;
XX arthritic wound healing; diabetes; skeletal muscle cells; obesity;
XX Berger disease; nephropathy; Schonlein-Henoch purpura; colliac disease;
XX dermatitis; herpeticiformis; Crohn's disease; thalassemia.
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 XX (GENT) GENENTECH INC.  
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 XX Baker KP, Borstein D, Desnoyers L, Eaton DL, Ferrara N, Fong S,  
 PI Gao W, Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,  
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 PI Williams PM, Wood WT;  
 XX  
 DR WPI, 2003-708395/67.  
 DR P-PSDB; ADE50596.  
 XX  
 XX Novel secreted and transmembrane PRO polypeptides useful in the  
 PT preparation of a medicament for treating a condition responsive to PRO  
 PT polypeptide and as therapeutic agents e.g. vaccines.  
 XX  
 PS Claim 2; SEQ ID NO 305; 555pp; English.  
 XX  
 CC The invention relates to an isolated PRO polypeptide (secreted or

Query Match 100.0%; Score 989; DB 9; Length 989;  
 Best Local Similarity 100.0%; Pred. No. 3,6e-156;  
 Matches 989; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 421 CGGGCTACTCG 480  
 QY 481 GCGAGGTGAGCG 540  
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QY	721	TCTGTGGCGGAGAGGTGCTGCAACCTCCGAAAGGGGACGTGGCGGCGGAGTGTGC	780
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Db	781	GAAACCTTAACGAAAGCATCCGCGGGAGCTCAGGGTCTACATCAGCCTCTGCCCCCTGG	840
QY	841	GCGATGAGACTCACCTTGCCCTTCAAGATCTAGGGCTGGCCCTAGTAGTGGGCTCGAGG	900
Db	841	GCGATGAGACTCACCTTGCCCTTCAAGATCTAGGGCTGGCCCTAGTAGTGGGCTCGAGG	900
QY	901	GAGGGTTGCTGGGAAACCCAGAAATTGACCCCTGAGTTTAAATTGAAAAATAAAGTGGG	960
Db	901	GAGGGTTGCTGGGAAACCCAGAAATTGACCCCTGAGTTTAAATTGAAAAATAAAGTGGG	960
QY	961	GCTGGGACACAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA	989
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Search completed: April 10, 2004, 14:16:08  
 Job time : 477 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd

OM nucleic - nucleic search, using sw model

Run on: April 10, 2004, 13:51:29 ; Search time 3083 Seconds  
(with about 31 arguments)

9579.532 Million cell updates/sec

Title: US-10-017-407A-305

Sequence: 1 ggcggcccgagtcgcgaga...caaaaaaaaaaaaaaaaaa 985

Scoring table: IDENTITY\_NUC

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026576

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: em_esthum:*
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14: gb_est5:*
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16: em_estom:*
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18: em_gss_inv:*
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## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	765.6	77.1	771	14	CB852030	CB852030 UT-CF-FNNO
3	743	75.1	814	18	BM051236	BM051236 603634199
4	736	74.4	756	14	CAV77547	CAV77547 IP21907.X

C	5	721	72.9	1006	10	BF663323	BF663323	602144463
C	6	716	72.4	9921	10	BF664198	BF664198	602145812
C	7	707.2	71.5	714	12	BM976177	BM976177	UI-CF-ENI
C	8	699.8	70.8	750	14	CB852718	UI-CF-ENI	CB852718
C	9	684.4	69.2	772	10	BE796670	601592247	BE796670
C	10	666.8	67.4	779	14	BF663695	602145414	BF663695
C	11	666.4	67.4	934	13	BQ931889	AGENCOCURT	BQ931889
C	12	630	63.7	1065	13	BM072803	AGENCOCURT	BM072803
C	13	625	63.2	1025	12	BM768764	K-ESTO051	BM768764
C	14	621	62.8	912	12	BG339939	602437508	BG339939
C	15	609.2	61.6	2243	11	AK054334	Mus muscu	AK054334
C	16	607.6	61.0	919	11	AK007659	Mus muscu	AK007659
C	17	603.4	61.0	906	10	AM157329	au94f01.x	AM157329
C	18	587.8	59.4	610	13	BY076594	BY076594	BY076594
C	19	585.8	59.2	589	9	A1692318	wd37h07.x	A1692318
C	20	585.6	59.2	1122	12	BG339915	602437607	BG339915
C	21	580	58.6	580	12	BM769685	K-ESTO052	BM769685
C	22	579	58.5	998	13	BQ918468	AGENCOCURT	BQ918468
C	23	578.4	58.5	581	9	A1929395	au95e03.y	A1929395
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C	25	574.6	58.1	904	14	CB194628	AGENCOCURT	CB194628
C	26	564.4	57.1	582	10	AM157252	au93e01.x	AM157252
C	27	562.8	56.9	886	14	CB181160	AGENCOCURT	CB181160
C	28	557.2	56.3	977	13	BT084188	AGENCOCURT	BT084188
C	29	549.2	55.5	578	9	AM003514	wq66g10.x	AM003514
C	30	548.6	55.5	620	9	AA544408	nm81b03.s	AA544408
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C	35	538.4	54.4	999	11	BC019647	Mus muscu	BC019647
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C	38	527.6	52.8	546	10	AM157459	au95h04.x	AM157459
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C	40	521.2	52.7	714	10	BF941318	602013260	BF941318
C	41	515.6	51.7	575	9	A1810740	tu04a11.x	A1810740
C	42	511.8	51.1	516	12	BG285119	602409396	BG285119
C	43	509.8	51.5	710	13	BO746381	UI-M-ERO-	BO746381
C	44	487.4	49.3	676	10	BB666437	BB666437	BB666437
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FEATURES  
source

Location/Qualifiers  
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/clone="IMAGE:549499"  
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/lab\_host="DH10B (phage-resistant)"  
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/note="Organ: eye; Vector: pCMV-SPORE6; Site: 1; NotI;  
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dN.  
Average insert size 1.75 kb. Library constructed by Life  
Technologies."

## ORIGIN

Query Match 80.6%; Score 797.4; DB 12; Length 889;  
Best Local Similarity 99.5%; Pred. No. 5.9e-89;  
Matches 821; Conservative 0; Mismatches 1; Indels 3; Gaps 2;

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DB 61 GGGCTAGCGGACATGGGGGCGCCCTTGCCCACTGAGCCCTTCTGAGGAGGCGGTGCCCC 120
QY 192 CCATGGCAGGCGCGGAGAGCAAGTGCCTGCTTCCCGGAGAGACCGCGCTGTGGAG 251
DB 121 CCATGGCAGGCGCGGAGAGCAAGTGCCTGCTTCCCGGAGAGACCGCGCTGTGGAG 180
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DB 181 TATCTTTCAGACCGCGTCCATGCGGAGAGACCGCGGCGCTGCGAGAGCTGAGGCTGAC 240
QY 312 CTGAGAGCAGCGCAGGGGAGATTCTATGATGACCTGCGAGAGCGCCACTTGTGGCCAC 371
DB 241 CTGAGAGCAGCGCAGGGGAGATTCTATGATGACCTGCGAGAGCGCCACTTGTGGCCAC 300
QY 372 CTGAGGCGGCTCATTCAGAGCCAGAGGCGCTGAGCCCTGAGCCACTTCAAGGCTACTCC 431
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DB 361 GCGCTGCGCCCTGAGCCCTGAGCGCTGCGCGAGACGGGCGCTGTGACCTTGCGAGGTGAC 420
QY 492 GCGCAGCGCGCGAGCTGAGAGCGGCTGCTGAGAGGAGCGCGGAGGCGGAGCAAGATC 551
DB 421 GCGCAGCGCGCGAGCTGAGAGCGGCTGCTGAGAGGAGCGCGGAGGCGGAGCAAGATC 480
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DB 481 GACCTCCGCGTGAAGCCCGCTTGGAGAGCTTGAAGAGCTGTGAGCGGCGGAGGCGC 540
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DB 541 GCGACCTTTCAGCTGAGCGGCTGAGTGGAGCAAGAGAACTGCTCCGCTACTAGAG 600
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RESULT 2  
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LOCUS UI-CF-FNO-aes-j-02-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone  
DEFINITION UI-CF-FNO-aes-j-02-0-UI 3', mRNA sequence.  
ACCESSION CB852030  
VERSION CB852030.1 GI:30046884  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Ronald M.F., Lennon, G. and Soares, M.B.  
TITLE 1 (bases 1 to 771)  
Normalizaton and subtraction: two approaches to facilitate gene  
discovery  
JOURNAL Genome Res. 6 (9), 791-806 (1996)  
MEDLINE 97044477  
PubMed 8889548

COMMENT  
McCray Lab  
Contact: McCray, PB

University of Iowa  
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA  
Tel: 319 356 4866  
Fax: 319 356 7171

Email: paul-mccray@iowa.edu  
Tissue Procurement: Dr. M. J. Welsh, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research  
Genetics (www.reagen.com).  
Seq primer: M13 FORWARD  
POLYA=Yes.

FEATURES  
source

Location/Qualifiers  
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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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modified polylinker; Site 1: EcoR I; Site 2: Not I;  
UI-CF-FNO is a subtracted cDNA library derived from two  
normalized Human Lung epithelial cell libraries (EN1 and  
DUI). The library was subtracted according to  
Bonaldio, Lennon and Soares, Genome Research, 6:791-806,  
1996. For additional information, contact:  
bento-soares@iowa.edu  
TAG\_SEQ=None found"

## ORIGIN

Query Match 77.1%; Score 762.6; DB 14; Length 771;  
Best Local Similarity 99.5%; Pred. No. 1.2e-84;  
Matches 765; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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QY 281 CCGGCGCTGCGAAGCTTGAAGCTGTGACCTCTGAGCAGCGCGGAGGAGATTATGAT 340
DB 711 CCGGCGCTGCGAAGCTTGAAGCTGTGACCTCTGAGCAGCGCGGAGGAGATTATGAT 652
QY 341 GACCTGAGAGCAGCGCAGCTTGTGCGAAGCTGAGCGGCTCATTCAGAGCAAGAGGC 400
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LOCUS  
DEFINITION  
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ACCESSION  
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VERSION  
CA777547.1 GI:26015422  
KEYWORDS  
EST.  
SOURCE  
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ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
Melson, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lentschka, I., Scaer, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Warr, M., Pape, D., Wyle, T., Martin, U., Blisstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, U., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, W., Williams, T., Jackson, Y., and Bowers, Y.,  
Williams, T., Jackson, Y., and Bowers, Y.,  
Endocrine Pancreas Consortium  
Unpublished (2000)  
CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
Endocrine Pancreas Consortium  
Harvard University, Howard Hughes Medical Institute  
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
Tel: 617-495-1812  
Fax: 617-495-8557  
Email: dmelton@biochem.harvard.edu  
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center for information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)  
Seq primer: -40UP from Gibco  
High quality sequence stop: 462.  
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/mol\_type="mRNA"  
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/clone\_id="HR85 islet"  
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site: 1: NotI; Site 2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN  
Query Match 74.4%; Score 736; DB 14; Length 756;  
Best Local Similarity 99.2%; Pred. No. 2,2e-81;  
Matches 750; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

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QY 582 CTGACGAGCTGCTGAGCGCGCGCGAGCGAGCGACCTTTCAGCTGAGCGCGGTGATCG 641  
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QY 702 ATCTGCGCGCTGCTGAGAGTCTGTGCGCGGAGGCTTGCACCTCCGAAAGGGAGC 761  
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QY 762 GTGGCGCGCGAGCTGTGTGCGAACTTAAAGCAAGCACTCCGCGGAGGTGAGGTCTAC 821  
DB 216 GTGGCGCGCGAGCTGTGTGCGAACTTAAAGCAAGCACTCCGCGGAGGTGAGGTCTAC 157  
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DB 156 ATCAGCTCTCTGCTGCGCGAGTGAAGTCACTTGTGAGCTTGAAGATTAAGGCTGAGC 97  
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RESULT 5  
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DEFINITION  
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ACCESSION  
BF663323  
VERSION  
BF663323.1 GI:11937218  
KEYWORDS  
EST.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE  
1 (bases 1 to 1006)  
NIH-MGC <http://mgi.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
Email: cgaab@remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: InCyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
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FEATURES  
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Db 776 GCCTCAGATCTAGAGGCTGGCC 797

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RESULT 7
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LOCUS UI-CF-EN1-acy-e-23-0-UI.s1 UI-CF-EN1 Homo sapiens cDNA clone
DEFINITION UI-CF-EN1-acy-e-23-0-UI 3', mRNA sequence.
ACCESSION BM976177
VERSION BM976177.1 GI:19593768
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 714)
AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and Subtraction: two approaches to facilitate gene
discoveary
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: McCray, PB
McCray Lab
University of Iowa
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mccray@iowa.edu

```

Tissue Procurement: Dr. M. J. Welch, University of Iowa  
 cDNA library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Researchers may obtain clones from Research  
 Genetics (www.resgen.com) or from Open Biosystems  
 (www.openbiosystems.com).  
 Seq primer: M13 FORWARD  
 POLYA=Yes

## FEATURES

## Source

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1..714
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-CF-EN1-acy-e-23-0-UI"
/tissue_type="Primary Lung Cystic Fibrosis Epithelial
Cells"
/dev_stage="Adult"
/lab_host="DH10B (life technologies) (T1 phage resistant)"
/clone_lib="UI-CF-EN1"
/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a
modified polylinker; Site 1: EcoR I; Site 2: Not I;
UI-CF-EN1 is a normalized cDNA library containing the
following tissue(s): Primary Lung Cystic Fibrosis
Epithelial Cells. The library was constructed according to
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. First strand cDNA synthesis was primed with an
oligo-dr primer containing a Not I site. Double stranded
cDNA was ligated to an EcoR I adaptor, digested with Not
I, and cloned directionally into pT7T3-Pac vector. The
oligonucleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is CTGCTCAGT.
TAG TISSUE=Human Lung Epithelial Cell Lines untreated LPS
6hr to LPS 24h
TAG LIB=UI-CF-EN1
TAG_SEQ=CTGCTCAGT"

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## ORIGIN

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Query Match 71.5%; Score 707.2; DB 12; Length 714;
Best Local Similarity 99.6%; Pred. No. 7,6e-78;
Matches 709; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 278 GACCCGCGCGCTGCGAGAGCTGAGCTGCTGACCTTGGAGAGAGCGGAGATTCTAT 337
Db 714 GACCCGCGCGCTGCGAGAGCTGAGCTGCTGACCTTGGAGAGAGCGGAGATTCTAT 655
Qy 338 GATGACCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 397
Db 654 GATGACCTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 595
Qy 398 GCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 457
Db 594 GCGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 535
Qy 458 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 517
Db 534 GCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 475
Qy 518 CCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 577
Db 474 CCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 415
Qy 578 GACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 637
Db 414 GACCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 355
Qy 638 TCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 697
Db 354 TCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 295
Qy 698 AGGCATCTCGCGCTGCTCAGAGTCTGTGCGCGGAGAGTGTGCAACTCCGAAAG 757

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Db 294 AGGCACTCTGCGCCCTCTCAGAGTCTGTGGCGGGAGAGTGTGCAACCTCCGAAGG 235

Qy 758 GGAGCTGGCGCGCCAGTGTGTGCGAAAACCTAAACGAACGATCCGGCGGACGTCAAGGT 817

Db 234 GGAGCTGGCGCGCCAGTGTGTGCGAAAACCTAAACGAACGATCCGGCGGACGTCAAGGT 175

Qy 818 CTAATCATGCTCTCTGCGCCCTGCGGAGTGAAGTCACTTGGCTTCAAGATCTAGGGCTG 877

Db 174 CTAATCATGCTCTCTGCGCCCTGCGGAGTGAAGTCACTTGGCTTCAAGATCTAGGGCTG 115

Qy 878 GCCCTAGTGAAGTGGCTCGAGGAGGCTTCTCTGGGAACCCAGAAATGACCCCTAGT 927

Db 114 GCCCTAGTGAAGTGGCTCGAGGAGGCTTCTCTGGGAACCCAGAAATGACCCCTAGT 55

Qy 938 TTTAAATTCGAAATTAAGTGGGCTGGGACACAAAAA 989

Db 54 TTTAAATTCGAAATTAAGTGGGCTGGGACACAAAAA 3

RESULT 8

LOCUS CB852718 750 bp mRNA linear EST 22-APR-2003

DEFINITION UI-CF-FNO-afl-p-08-0-UI.s1 UI-CF-FNO Homo sapiens cDNA clone

ACCESSION CB852718

VERSION CB852718.1 GI:30047716

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 750)

AUTHORS Bonaldo,M.F., Lennon,G. and Soares,M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery

JOURNAL Genome Res. 6 (9), 791-806 (1996)

MEDLINE 97044477

PUBMED 8889548

COMMENT Contact: McCray, PB

McCray Lab

University of Iowa

2024 University of Iowa Med Labs, Iowa City, IA 52242, USA

Tel: 319 356 4866

Fax: 319 356 7171

Email: paul.mccray@uiowa.edu

Tissue Procurement: Dr. M. J. Welsh, University of Iowa

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa

cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com) or from Open Biosystems (www.openbiosystems.com).

Seq primer: M13 FORWARD

POLYA-No.

# FEATURES

Source

1. .750

Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="UI-CF-FNO-afl-p-08-0-UI"

/tissue="Human Lung Epithelial cells"

/lab\_host="DH10B (Life Technologies) (T1 phage resistant)"

/clone\_id="UI-CF-FNO"

/note="Organ: Lung; Vector: pT73-Pac (Pharmacia) with a modified polylinker; Site 1: Ecor I; Site 2: Not I; UI-CF-FNO is a subtracted cDNA library derived from two normalized Human lung epithelial cell libraries (EN1 and DUI) The library was subtracted according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. For additional information, contact: bento-soares@uiowa.edu

TAG\_SEQ=None found"

## ORIGIN

Query Match 70.8%; Score 699.8; DB 14; Length 750;  
Best Local Similarity 97.3%; Pred. No. 6,1e-77;  
Matches 732; Conservative 0; Mismatches 18; Indels 2; Gaps 2;

Qy 148 GGGCGCCCTTCCGCACTGGCCCTTCTCTGGGAGGCGTGTCCCGCAAGAGCCGCG 207

Db 1 GGGCGCGCTCAACACCCCTCTCCCGTCAAGGAGGCGTGTCCCGCAAGAGCCGCG 60

Qy 208 GAGAGAGTGTCTGTCTCCCGCGAGAGAGCGGCGCTGTGAGATCTTCTGACCGCT 267

Db 61 GAGAGAGTGTCTGTCTCCCGCGAGAGAGCGGCGCTGTGAGATCTTCTGACCGCT 120

Qy 268 CCATGCGGAGACACCGCGCTGTGCAAGCTTGAAGCTGTGACCTGTGAGAGCGCGAG 327

Db 121 CCATGCGGAGACACCGCGCTGTGCAAGCTTGAAGCTGTGACCTGTGAGAGCGCGAG 180

Qy 328 GGGATTCATATGATGACCTGCGAGAGGCGAGGCTTGTGGCCAACTGGGCGGCTCATCC 387

Db 181 GGGATTCATATGATGACCTGCGAGAGGCGAGGCTTGTGGCCAACTGGGCGGCTCATCC 240

Qy 388 AGGCCAAGAGCGGCTGTGACCTGTGACCGCTTGTGACCGGCTTGTGACCGCTGTGACCG 447

Db 241 AGGCCAAGAGCGGCTGTGACCTGTGACCGCTTGTGACCGGCTTGTGACCGCTGTGACCG 300

Qy 448 TGGCGCTGCGCGCGAGCGGCGGCTGTGACCTGTGACCGGCTTGTGACCGGCTTGTGACCG 507

Db 301 TGGCGCTGCGCGCGAGCGGCGGCTGTGACCTGTGACCGGCTTGTGACCGGCTTGTGACCG 360

Qy 508 TGGGACGCGCCCTGTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 567

Db 361 TGGGACGCGCCCTGTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 420

Qy 568 CCGCCTTGTGAGACCTGTGAGAGGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 627

Db 421 CCGCCTTGTGAGACCTGTGAGAGGCTGTGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480

Qy 628 CCGTGTGTGATGCGGACAAAGAGAACTGTGCGGCTTGTGAGAGGCGGCGGCGGCGGCGG 687

Db 481 CCGTGTGTGATGCGGACAAAGAGAACTGTGCGGCTTGTGAGAGGCGGCGGCGGCGGCGG 540

Qy 688 TCGGACCGCGAGGACCTCTGCGGCTTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 747

Db 541 TCGGACCGCGAGGACCTCTGCGGCTTGTGAGAGGCGGCGGCGGCGGCGGCGGCGGCGG 600

Qy 748 CTCGGAAGGAGGAGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 807

Db 601 CTCGGAAGGAGGAGCGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660

Qy 808 ACGTACGAGGTCTACATCAAGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 867

Db 661 ACGTACGAGGTCTACATCAAGCTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 719

Qy 868 TCTAGGCTGCGCCCTTGTGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 899

Db 720 TCTAGGCTGCGCCCTTGTGAGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 750

RESULT 9

LOCUS BE796570 772 bp mRNA linear EST 20-SEP-2000

DEFINITION 6015922471 NIH\_MGC\_7 Homo sapiens cDNA clone IMAGE:3946546 5',

ACCESSION BE796570

VERSION BE796570.1 GI:10217768

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 772)

AUTHORS NIH-MGC http://mgi.nci.nih.gov/.

TITLE  
JOURNAL  
COMMENT

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@db-remail.nih.gov  
Tissue Procurement: DCTD/DRP  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: [image.llnl.gov](http://image.llnl.gov)  
Plate: LNCM806 row: m column: 11  
High quality sequence stop: 766.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:3946546"  
/tissue\_type="small cell carcinoma"  
/cell\_line="MGC3"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH MGC 7"  
/note="Organ: Lung; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

## ORIGIN

Query Match 69.2%; Score 684.4; DB 10; Length 772;  
Best Local Similarity 97.4%; Pred. No. 4.7e-75;  
Matches 760; Conservative 0; Mismatches 11; Indels 9; Gaps 6;

83 CATGACCCAGCCGCGTCCCGGCTCTCCCGGCGCGCTGAGCCTGAGGCTCAGCGC 142  
1 CATGACCCAGCCGCGTCCCGGCTCTCCCGGCGCGCTGAGCCTGAGGCTCAGCGC 60.  
143 ACTGGGCGCGCTTGGCACTGAGCTTCTTCTGGGAGAGCGGCTGCGCCCGATGCGAG 202  
61 ACTGGGCGCGCTTGGCACTGAGCTTCTTCTGGGAGAGCGGCTGCGCCCGATGCGAG 120  
203 CCGGAGAGAGAGTGGCTTCCCGGCGAGAGAGCGCTGAGGAGTATCTTCTGAG 252  
121 CCGGAGAGAGAGTGGCTTCCCGGCGAGAGAGCGCTGAGGAGTATCTTCTGAG 180  
263 CCGCTCCATGCGGAGAGAGCGCGGCTGCGAGGCTGAGGCTGAGCCTGAGAGAGCC 322  
181 CCGCTCCATGCGGAGAGAGCGCGGCTGCGAGGCTGAGGCTGAGCCTGAGAGAGCC 240  
323 GAGGGGATTTCTATGATGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 352  
241 GAGGGGATTTCTATGATGACCTGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300  
383 CATCAGAGCCAAAG 442  
301 CATCAGAGCCAAAG 360  
443 GAGCTGAGCGTCCCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 502  
361 GAGCTGAGCGTCCCGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420  
503 GAGCTGAG 552  
421 GAGCTGAG 480  
563 GAGCTGAG 622  
481 GAGCTGAG 538  
623 GAGCTGAG 682

Db 539 CTTGGCCCTGTGTGATGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598  
QY 683 GCTGCTGAG 742  
Db 599 GCTGCTGAG 658  
QY 743 GC-AACCTCGAAG 801  
Db 659 GCAACCTCGAAG 715  
QY 802 GAGGAG 861  
Db 716 GAGGAG 772

RESULT 10  
BF663695 779 bp mRNA linear EST 21-DEC-2000  
LOCUS 602145414F1 NIH\_MGC\_48 Homo sapiens cDNA clone IMAGE:4309010 5',  
DEFINITION mRNA sequence.  
ACCESSION BF663695  
VERSION BF663695.1 GI:11937590  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
1 (bases 1 to 779)  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@db-remail.nih.gov  
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.  
cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <http://image.llnl.gov>  
Plate: LNCM181 row: 1 column: 03  
High quality sequence stop: 761.  
Location/Qualifiers

## FEATURES

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/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4309010"  
/tissue\_type="Primary B-cells from tonsils (cell line)"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_1ib="NIH MGC 48"  
/note="Organ: B-cells; Vector: pORF7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).  
Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 67.7%; Score 669.8; DB 10; Length 779;  
Best Local Similarity 98.1%; Pred. No. 2.9e-73;  
Matches 762; Conservative 0; Mismatches 7; Indels 8; Gaps 8;

79 GGGCCATACCCAGAGCGGCTTCCCGGCTCTCCCGGCGCGCTGAGCCTGAGGCTAG 138  
Db 2 GGGCCATACCCAGAGCGGCTTCCCGGCTCTCCCGGCGCGCTGAGCCTGAGGCTAG 61  
QY 139 CCGCACTGAGCGCGCTTGGCACTGAGCTTCTTCTGGGAGAGAGCGGCTGAGCCT 198

Db	52	CGGCACTGGGGCGCCGCTTTCGGCACTGGGCTCTTCTCGGGAGAGGGGGTCCGCCCATGAC	121
QY	199	GAGGCGGGCGAGAGAGTGGCTGCTCTTCCCCCGAGAGACAGCCGCTGTGGCAGTATCTTC	258
Db	122	GAGGCGGGCGAGAGAGTGGCTGCTCTTCCCCCGAGAGACAGCCGCTGTGGCAGTATCTTC	181
QY	259	TGAGCGGCTCCATGGCGGAGACACCGGCGCTCGAAGCCTGAGGCTGTGACCTCGAGAC	318
Db	152	TGAGCGGCTCCATGGCGGAGACACCGGCGCTCGAAGCCTGAGGCTGTGACCTCGAGAC	241
QY	319	AGCCCGAGGGGAGATTCTATGATGACCTGCGACA-GGCCAGCTTTTGCCAACTTGAC-376	
Db	242	AGCCCGAGGGGAGATTCTATGATGACCTGCGACATGGCCAGGCTTTTGCCAACTTGACCT	301
QY	377	GCGGCTCATCCAGGGCGAAGAGGGGCTGGACCTTGAGGACCTTTAC-GGGCTATCTCGGCG	435
Db	302	GCGGCTCATCCAGGGCGAAGAGGGGCTGGACCTTGAGGACCTTTACCTTGAGGCTCGGCG	361
QY	436	TGGCCCTGGCCCTTGAC-GCTGCCCGCGAGACGGGCGCGTGTGATCTCGAGGTGGACGCG	494
Db	362	TGGCCCTGGCCCTTGACCTTGCTGCTGCCGCGAGCGGGCGCGTGTGATCTCGAGGTGGACG	421
QY	455	CAGCCCCCGGAGCTTGGAGAGGCTTGTGGAGGCGGCTCGAGGCGAGACCAAGATCGAC	554
Db	422	CAGCCCCCGGAGCTTGGAGAGGCTTGTGGAGGCGGCTCGAGGCGAGACCAAGATCGAC	481
QY	555	CTCCGGCTGGAAGCCCGCTTGGAGACCTTGACGAGCTGTGGCGGCGAGGCGGCGCG	614
Db	482	CTCCGGCTGGAAGCCCGCTTGGAGACCTTGACGAGCTGTGGCGGCGGCGGCGGCGCG	541
QY	615	ACCTTCGACGTGGCCCGTGTGT-GGATCGGACAGAGGAACTTGCTCCGCTACTACGACG	673
Db	542	ACCTTCGACGTGGCCCGTGTGTGGAGATGCGAGACAGAGGAACTTGCTCCGCTACTACGACG	601
QY	674	CTGCGCTGAGCTGTGGACCCCGGAGGAG-TCCTGGCCGCTCTAGATCTCTTGGAGCGG	732
Db	602	CTGCGCTGAGCTGTGTGGACCCCGGAGGAGATTCCTTGCCGCTCTAGATCTTGTGGAGCG	661
QY	733	GGAAGTGTCTGTGAACCTTCGGAAGGGGAC-GTGGCGGCGGAGTGTGTGCGAACTTAAC	791
Db	662	GGAAGTGTCTGTGAACCTTCGGAAGGGGACGCGTGGCGGCGGAGTGTGTGCGAACTTAAC	721
QY	732	GAGCCCATCCGGCGGGGAC-GTTCAGGGCTTACATCAGCCTCTGCGCCCTGGGCGATGG	847
Db	722	GACCGCATCCGGCGGGGACCGTTCAGGGCTTACATCAGCTTGTGGCCCTTGGCCGATGG	778
RESULT 11			
BO931589 934 bp mRNA linear EST 21-NOV-2002			
LOCUS BO931589 AGENCOURT_8795361 NIH_MGC_101 Homo sapiens cDNA clone IMAGE:642775			
DEFINITION 5', mRNA sequence.			
ACCESSION BO931589			
VERSION BO931589.1 GI:22346620			
KEYWORDS EST.			
ORGANISM Homo sapiens (human)			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
1 (bases 1 to 934)			
NIH-MGC http://mgi.nci.nih.gov/.			
National Institutes of Health, Mammalian Gene Collection (MGC)			
Unpublished (1999)			
COMMENT			
JOURNAL			
TITLE			
AUTHORS			
REFERENCE			
CNSA Library Preparation: Rubin Laboratory			
DNA Sequencing by: Agencourt Bioscience Corporation			
Clone distribution: MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/ILNI at:			
http://image.jnl.gov			
Plate: ILNCM2613 row: e column: 24			

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FEATURES
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                /note="Organ: Lung; Vector: pOTB7; Site.1: EcoRI; Site.2:
                XhoI; cDNA made by oligo-dT priming. Directionally cloned
                into EcoRI/XhoI sites using the following 5' adaptor:
                GGCCAGAG(G). Library constructed by Ling Hong in the
                laboratory of Gerald M. Rubin (University of California,
                Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                Superscript II RT (Life Technologies). Note: this is a
                NT1_MGC Library."

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	Query Match	97.4%	Score 666.4	DB 13	Length 934
	Best Local Similarity	95.8%	Pred. No. 7,38-73		
	Matches 751	Conservative	0	Mismatches 21	Indels 12
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QY	87	ACCCAGCCGGTGC	CCCGGCTCTCGGTGC	CCGCGCGCTTGCCCTTCAAGCCGAC	CTG 145
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QY	147	GGGCGCGCTTGGCC	CACTGCGCTCTTCTGGGGA	GGGGTGGCCCCCA	TGGCGAGGCCG 206
Db	61	GGGCGCGCTTGGCC	CACTGCGCTCTTCTGGGGA	GGGGTGGCCCCCA	TGGCGAGGCCG 120
QY	207	CGAGACAGATGCTCT	CTTCCCCCGAGAGACAG	CGCGCTGTGACGATCTTCTGACCGC	266
Db	121	CGAGACAGATGCTCT	CTTCCCCCGAGAGACAG	CGCGCTGTGACGATCTTCTGACCGC	180
QY	267	TCCATGCGGAGAC	CCGCGCTGTGAGCCTGAGGCTGTGA	CCTGAGACGCCGAG	326
Db	181	TCCATGCGGAGAC	CCGCGCTGTGAGGCTGTGA	---GCTGACCTGAGACGCCGAG	236
QY	327	GGGGATTTATATATA	CTTGGAGAGAGCCCA	GTCTTTGGCCAACTGGGGCGGCTCATC	386
Db	237	GGGGATTTATATATA	CTTGGAGAGAGCCCA	GTCTTTGGCCAACTGGGGCGGCTCATC	296
QY	387	CAGGCCAAGAGAGCG	CTGAGACCTTCA	CGGAGCTAC	TCGCGCCCTGGCCCTGAGC 446
Db	297	CAGGCCAAGAGAGCG	CTGAGACCTTCA	CGGAGCTAC	TCGCGCCCTGGCCCTGAGC 356
QY	447	CTTGGCGCTGCCCG	CGAGCGGCGCGTGTGA	CTTCAAGGTGAGACGCGACGCCCGGAG	506
Db	357	CTTGGCGCTGCCCG	CGAGCGGCGCGTGTGA	CTTCAAGGTGAGACGCGACGCCCGGAG	416
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Db	417	CTTGGACGCGCCCT	TGTGAGGCAAGCCGAGCGGAGAC	CAAGATCACTTCGCGGTGAAG	476
QY	567	CCGCGCTTGAAGAC	CTTGAAGAGGCTGTGCGCGGAGCGGAGC	CACTTCAAGCTG 626	
Db	477	CCGCGCTTGAAGAC	CTTGAAGAGGCTGTGCGCGGAGCGGAGC	CACTTCAAGCTG 536	
QY	627	GCCTGTGTGATGCG	AGAGAGAACTCTCCGCTTCA	ACGAGCGCTGCTGACCTG 686	
Db	537	GCCTGTGTGATGCG	AGAGAGAACTCTCCGCTTCA	ACGAGCGCTGCTGACCTG 596	
QY	687	CTTGGACCCGAGAG	CAATCTTGCGCTTCA	GAATCTTGCGCGGAGAGGCTGCA 746	
Db	597	CTTGGACCCGAGAG	CAATCTTGCGCTTCA	GAATCTTGCGCGGAGAGGCTGCA 656	
QY	747	CTTCCGAAAGGAGAG	CTTGGCGCGAGTGTGTG	CGAACTTAAACGACGC--ATCC 801	
Db	657	CTTCCGAAAGGAGAG	CTTGGCGCGAGTGTGTG	CGAACTTAAACGACGCATCCG 716	
QY	802	GGCGGAGCGTCA	GGGTCTAATCAAGCTCTCTG	---CCCTGGGCGATGACTCACTTGG 858	

Db 717 GCGGGAGAGTACAGGGTCTATACAGCTCCCGGCGCTGGGCGAAGGAGTCACTG 776  
 QY 859 CCTT 862  
 Db 777 CCTT 780

## RESULT 12

BO072503 1065 bp mRNA linear EST 02-APR-2002  
 LOCUS BO072503  
 DEFINITION AGENCOURT 6838941 NIH\_MGC\_122 Homo sapiens cDNA clone IMAGE:5761696  
 5'..mRNA sequence.

ACCESSION BO072503  
 VERSION BO072503.1 GI:19901549  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE NIH-MGC http://mgs.nci.nih.gov/  
 1 (bases 1 to 1065)

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.

Email: cgsab@remail.nih.gov  
 Tissue Procurement: Life Technologies, Inc.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM12810 row: 1 column: 17  
 High quality sequence stop: 489.

## FEATURES

Location/Qualifiers

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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5761696"  
 /lab\_host="DH10B"  
 /clone\_id="NIH\_MGC\_122"  
 /note="Organ: pooled lung and spleen; Vector: pCMV-SPORT6;  
 Site 1: NotI; Site 2: EcoRV (destroyed); RNA source  
 anonymous pool of 24 week female lung; 16 week female  
 spleen, and 20-22 week male spleens. Library is oligo-dT  
 primed, and directionally cloned (EcoRV site is destroyed  
 upon cloning). Average insert size 1.4 Kb, insert size  
 range 1-3 Kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 026. Note:  
 this is a NIH\_MGC Library."

## ORIGIN

Query Match 63.7%; Score 630; DB 13; Length 1065;  
 Best Local Similarity 96.7%; Pred. No. 2,1e-68;  
 Matches 675; Conservative 0; Mismatches 20; Indels 3; Gaps 3;

QY 1 GCGGGCGCGAGTCCGAGACCTGTCCAGAGAGTCCAGTCACTGACTGTACCTGCC 60  
 Db 1 GCGGGCGCGAGTCCGAGACCTGTCCAGAGAGTCCAGTCACTGACTGTACCTGCC 60  
 QY 61 TCCGCGCGCTCTCTGCGCGCGCCATGAGACCCGCGTCCGCTCCGCGCGCGCG 120  
 Db 61 TCCGCGCGCTCTCTGCGCGCGCCATGAGACCCGCGTCCGCTCCGCGCGCGCG 120  
 QY 121 GCGTGGCGCTGAGCGGAGTGGGCGCGCTTGGCCAGTGGCTCTTCTTGGGGA 180  
 Db 121 GCGTGGCGCTGAGCGGAGTGGGCGCGCTTGGCCAGTGGCTCTTCTTGGGGA 180  
 QY 181 GCGCGTGGCGCGGAGGCGCGGAGAGAGAGTGGCTTCCCGCGAGAGACAGCC 240

Db 181 GCGCGTGGCGCGGAGGCGCGGAGAGAGAGTGGCTTCCCGCGAGAGACAGCC 240  
 QY 241 GCGTGGAGATATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCTGGAGACCTGA 300  
 Db 241 GCGTGGAGATATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCTGGAGACCTGA 300  
 QY 301 GCGTGGAGATATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCTGGAGACCTGA 360  
 Db 301 GCGTGGAGATATCTTCTGAGCGCGCTCCATGCGGAGACACCGCGCTGGAGACCTGA 360  
 QY 361 TCTTGGCGCACTGGGCGCGGCTCATCGAGCCAGAGAGGCGTGGACCTTCA 420  
 Db 361 TCTTGGCGCACTGGGCGCGGCTCATCGAGCCAGAGAGGCGTGGACCTTCA 420  
 QY 421 CGGCTACTCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 480  
 Db 421 CGGCTACTCGCGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCTTGGCT 480  
 QY 481 GCGAGGTGAGCGCGAGCGCGCGCGGAGCTGGAGCGCGCTTGGAGAGCGCGAGCGG 540  
 Db 481 GCGAGGTGAGCGCGAGCGCGCGCGGAGCTGGAGCGCGCTTGGAGAGCGCGAGCGG 540  
 QY 541 AGCAGAGATGACCTCGCGCTGAAAGCCCGCTTGAAG-CCCTGAGAGAGCTGTGCG 599  
 Db 541 AGCAGAGATGACCTCGCGCTGAAAGCCCGCTTGAAG-CCCTGAGAGAGCTGTGCG 599  
 QY 600 G-CGCGCGAGCGCGGCA-CTTTCAGAGCGCGCTGTGTGAGGAGAGAGAGAGAGAGAG 657  
 Db 601 GACGGCGAGCGCGGAGCGCGCTTGAAGGCGCGTGTGTGAGGAGAGAGAGAGAGAGAG 660  
 QY 658 CGGCTACTGAGAGCGCGCTGCGCTGAGCTGTGCGAGCC 695  
 Db 661 CCGCTACTGAG 698

## RESULT 13

BM768764 625 bp mRNA linear EST 04-MAR-2002  
 LOCUS K-EST0051789 S14K402 Homo sapiens cDNA clone S14K402-11-A01 5',  
 DEFINITION mRNA sequence.

ACCESSION BM768764  
 VERSION BM768764.1 GI:19098379  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,  
 Oh, K.J., Cheong, Y.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and  
 Kim, Y.S.  
 21C Frontiers Korean EST Project 2001  
 Unpublished (2002)  
 Contact: Kim YS

## TITLE

JOURNAL

Genome Research Center  
 Korea Research Institute of Bioscience & Biotechnology  
 52 Beon-dong, Yuseong-gu, Daejeon 305-333, South Korea  
 Tel: +82-42-860-4470  
 Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr  
 Plate: 11 row: A column: 01  
 High quality sequence stop: 625.

## FEATURES

Location/Qualifiers

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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
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 /note="Organ: Stomach; Vector: pTZ18RP1; Site 1: EcoRI;  
 Site 2: NotI; The poly (A) + RNA was dephosphorylated with



bacterial alkaline phosphatase (BAP) and then deacapped with taccaco acid pyrophosphatase (TAP). The deacapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dt-selected mRNA by priming with dt-tailed vector. The dt-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoR I which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10<sup>+</sup> by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

# ORIGIN

Query Match 63.2%; Score 625; DB 12; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1e-67;  
Matches 625; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	65	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	124
DB	1	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	60
QY	125	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	184
DB	61	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	120
QY	185	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	244
DB	121	GGCGCTCTGCGCGCCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCT	180
QY	245	GTGCGAGATCTTCTGAGCGGCTCCATCGGAGACCCCGCGCTGCGAGCT	304
DB	181	GTGCGAGATCTTCTGAGCGGCTCCATCGGAGACCCCGCGCTGCGAGCT	240
QY	305	GCTGACCTTGAGAGCGCGCGGATTTATGATGACCTGCGAGCGCCAGCT	364
DB	241	GCTGACCTTGAGAGCGCGCGGATTTATGATGACCTGCGAGCGCCAGCT	300
QY	365	GGCGACCTGCGCGGCTCATCGAGCGGAGCGGTCGAGACCTTCAGCGG	424
DB	301	GGCGACCTGCGCGGCTCATCGAGCGGAGCGGTCGAGACCTTCAGCGG	360
QY	425	CTACTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT	484
DB	361	CTACTCCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT	420
QY	485	GCTGAGCGGAGCGCGCGGAGCGGAGCGGCTGCGGAGCGGAGCGGAG	544
DB	421	GCTGAGCGGAGCGCGCGGAGCGGAGCGGCTGCGGAGCGGAGCGGAG	480
QY	545	CAAGATGACCTGCGGCTGGAAGCCGCTTGAAGACCTTGAAGAGCTG	604
DB	481	CAAGATGACCTGCGGCTGGAAGCCGCTTGAAGACCTTGAAGAGCTG	540
QY	605	CGAGCGCGGAGCTTCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGG	664
DB	541	CGAGCGCGGAGCTTCTGAGCGGCTGCGGCTGCGGCTGCGGCTGCGG	600
QY	665	CTACGAGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG	689
DB	601	CTACGAGCGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGG	625

RESULT 14  
BG339399 912 bp mRNA linear EST 27-FEB-2001  
LOCUS 602437508F1 NIH\_MGC\_46 Homo sapiens cDNA clone IMAGE:4555609 5',  
DEFINITION mRNA sequence.  
ACCESSION BG339399  
VERSION BG339399.1 GI:13145837  
KEYWORDS EST.

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 912)  
AUTHORS NIH-MGC  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strauberg, Ph.D.  
Email: cgaabs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Ling Hong/Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LHC1256 row: 0 column: 02  
High quality sequence stop: 719.  
Location/Qualifiers  
1. 912

## FEATURES

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/clone\_id="NIH\_MGC\_46"  
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dt priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 62.8%; Score 621; DB 12; Length 912;  
Best Local Similarity 96.5%; Pred. No. 2.8e-67;  
Matches 742; Conservative 0; Mismatches 15; Indels 12; Gaps 10;

QY	73	CTGCGCGCGCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCTG	132
DB	2	CTGCGCGCGCATGACCCAGCGGTCGCGGCTCCGCGCGCGCGCTG	61
QY	133	GCTCAGCGGAGCGGCGGCTTGGCACTGCGGCTCTGCGGAGAGCGG	192
DB	62	GCTCAGCGGAGCGGCGGCTTGGCACTGCGGCTCTGCGGAGAGCGG	121
QY	193	CATGCGGAGCGGCGGAGAGAGTGCTGCTTCCCGCGAGAGACCGCT	252
DB	122	CATGCGGAGCGGCGGAGAGAGTGCTGCTTCCCGCGAGAGACCGCT	181
QY	253	ATCTTGAGCGGCTCATGCGGAGAGCGGAGCGGCTGCGGAGCGGCT	312
DB	182	ATCTTGAGCGGCTCATGCGGAGAGCGGAGCGGCTGCGGAGCGGCT	241
QY	313	TGAGAGCGGCGGAGGAGATTTATGATGACCTGCGAGAGCGGAGCT	372
DB	242	TGAGAGCGGCGGAGGAGATTTATGATGACCTGCGAGAGCGGAGCT	301
QY	373	TGAGCGGCGCTCATGCGGAGAGAGCGGCTGCGAGAGCGGAGCT	432
DB	302	TGAGCGGCGCTCATGCGGAGAGAGCGGCTGCGAGAGCGGAGCT	361
QY	433	CCCTGCGCTTGGCGCTGCGGCTGCGGAGCGGCGCTGCTGAGCTG	492
DB	362	CCCTGCGCTTGGCGCTGCGGCTGCGGAGCGGCGCTGCTGAGCTG	420
QY	493	CGAGCGCGGAGAGCTGCGGAGCGGCTTGTGAGAGGAGCGGAGCG	552



Db 421 CGACAGCCCCGAGAGCTGGAGCG-CCTGTGTAGAGGACGCCGAGCGGAGACAAAGTCG 479

Qy 553 ACCCTCCGCTGAAGACCCCTTGGAGACCTCTGAGACAGCTCTGCGCGCGAGCGCG 612

Db 480 ACCCTCCGCTGAAGACCCCTTGGAGACCTCTGAGACAGCTCTGCGCGCGAGCGCG 539

Qy 613 GCACCTTGAAGCTGGCTGGTGGATGGCGCAAGAGAACTGCTCCGCTCTACTAGCAG 672

Db 540 GCACTTGAAGCTGG-CGTGTGGATGGCGCAAGAGAACTG--TTCGCTACTACAGC 596

Qy 673 GCTGCTTGAAGCTGGTGGAGCCCGAGGACATCTGCGCTCTGAGATCTGCGCG 722

Db 597 GCTG-CTGACAGCTGTGGGA-CGGAGGACATCTGCGCTCTGAGATCTGCGCG 654

Qy 723 GGAAGTGTGCTGCACTCCGAAAGGAGCGTGGCGCGCGAGTGTGTGCGAAACCTAAAG 792

Db 655 GGAAGTGTGCTGCA-CTCGAAAGGAGCGTGGCGG-CGAGTGTGTGCGAAAC--TAAAG 710

Qy 793 AAGCATCCGCGGAGACCTGAGAGCTTCAATCAGTCTGCTGCGCTGCG 841

Db 711 AAGCAT-CGGCGGAGCGTCAAGGCTCTACATCAGCTCTGCGCTGCG 758

RESULT 15

AK054334 2243 bp mRNA linear HTC 20-SEP-2003

LOCUS AK054334.1 GI:26344156

DEFINITION Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330016L21 product:weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus], full insert sequence.

ACCESSION AK054334

VERSION AK054334.1 GI:26344156

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

REFERENCE 1 Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999)

JOURNAL MEDLINE 99279253

PUBMED 10349636

REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, Y., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL MEDLINE 20499374

PUBMED 11042159

REFERENCE 3 Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, U., Nishi, K., Kitenuma, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Obara, E., Matsumi, M., Yoshida, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, T., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL MEDLINE 20530913

PUBMED 11076861

REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the PANTOM Consortium. Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)

JOURNAL MEDLINE 5

PUBMED

REFERENCE The PANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2243)

AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, M., Kondo, S., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Nunazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toy, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshinide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ Location/Qualifiers

FEATURES

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molecule="mRNA"

strain="C57BL/6J"

db\_xref="PANTOM DB:E330016L21"

db\_xref="MGI:2426440"

db\_xref="taxon:10090"

clone="E330016L21"

sex="female"

tissue\_type="ovary"

clone\_id="RIKEN full-length enriched mouse cDNA library"

dev stage="2 days pregnant adult"

40..828

note="unlabeled protein product; putative weakly similar to PUTATIVE O-METHYLTRANSFERASE (FRAGMENT) [Rhodothermus marinus] (SPT:Q9XCB8), evidence: FASTY, 55.5%ID, 97.3%length, match=331"

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db\_xref="GI:26344157"

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2223..2228

note="putative"

2243

note="putative"

ORIGIN

Query Match 61.6%; Score 609.2; DB 11; Length 2243;

Best Local Similarity 80.9%; Pred. No. 6, 2e-66;

Matches 723; Conservative 0; Mismatches 168; Indels 3; Gaps 1;

Qy 63 CCGCGGCTCTGCGCGCGCGCATGACCGCGCGCGCGCGCTGCGCGCGCGCG 122

Db 19 CCGCGGCTCTAAGCGACGACGAGCGCGCGCGCGCGCTGCTCTGCGCGCG 78

Qy 123 CTGGCCCTGGGCTGAGCGCGCGCGCGCGCTTCTGCGCGCGCGCGCGCG 182

Db 79 CTGGCCCTGGGCTGGGCGCGCTGGGCGCGCTTCGCTACTGCTCTTCTGCTGGGAAA 138  
QY 183 CGGTGCCCCCATGGCCGAGGCGCGGAGAGCAGTGCCTTCCCGCCGAGGACAGCGCG 242  
Db 139 CGGTGGCTCTCATGGGGGTCCAGGCGGAGAGCGCTCTGCTCCACTGAGGACATCC 198  
QY 243 CTGTGGCAGTATCTTCTGAGCGCTCCATGCGGAGGACCCGCGCTGCGAAGCTGAGG 302  
Db 199 CTGTGGCAGTATCTGCTAGCGCTCCATGAGAGGACCCGCGCTGCGGAGCTGCGA 258  
QY 303 CTGCTGACCTTGGAGGAGCGGAGGGATCTATGATGACCTTGGAGCAGGCCAGCTC 362  
Db 259 CTGCTGACCTTGGAGGAGCGGAGGGATTCATGATGACCTTGGACAGGCCAGCTT 318  
QY 363 TTGGCCAACTGGCGCGGCTTCATCAGGCCAAGAGGCGCTGACCTGGGCACCTTCAGC 422  
Db 319 CTGGCCAACTGGCGCGGCTCATTAAGGCCAAGAAAGCTGATCTGGGTACTTTCAGC 378  
QY 423 GGCTAATCCGCGCTGGCGCTTGGCGCTGCGCGTGGCGGAGCGGCGCTGCTGACCTGC 482  
Db 379 GGCTAATCCGCGCTGGCGCTTGGCGCTTGGCGCTTGGCGGCTGGCGGCTGGCGGCTGC 438  
QY 483 GAGGTGACGCGCGCGCGCGCGCGAGCTGGGAGCGCGCGCTGAGGAGCGCGAGCGGAG 542  
Db 439 GAGGTGACGCGAGGCGCGCGCGCGAGCTGGGAGCGCGCATGAGGAGCAGGAGAGTGGAG 498  
QY 543 CACAAGATCGACTTCGCGCTGAGCGCGCTTGGAGACCTTGAACGAGCTGCTGGCGCG 602  
Db 499 CAGAAGATCGACTTCGCGCTGAGCGCGCGCTGGCAGACATGAGTGAAGCTCTTACGCGCG 558  
QY 603 GCGGAGGCG 662  
Db 559 GCGGAGGCG 618  
QY 663 TACTACGAGCGCTGCTGAGCTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 722  
Db 619 TACTACGAGCGCTGCTGAGCTGCTGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 678  
QY 723 CTGTGGGCGCGGAGAGTGTGCTGCAACTCCGAAAGGAGGAGCGTGGCGCGCGAGTGTGCGA 782  
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QY 783 AACCTAAACGAGCGCATCCGCGCGGAGCGTCAAGGCTTACATCAAGCTCTGCGCGCTGGGC 842  
Db 739 AACCTGAACGAGCGCATCCGAGGAGCGCGAGGTTCATCAAGCTCTGCGCGCTGGAT 798  
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QY 903 GGGTGGCTTGGGAGACCCGAGGATTTGACCTGAGTTTAATTGAAATTAAG 956  
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Job time : 3089 secs